

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization  
International Bureau



(43) International Publication Date  
13 June 2002 (13.06.2002)

PCT

(10) International Publication Number  
**WO 02/46467 A2**

(51) International Patent Classification<sup>7</sup>: **C12Q 1/68**

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(21) International Application Number: PCT/IB01/02811

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(22) International Filing Date: 7 December 2001 (07.12.2001)

(25) Filing Language: English

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(26) Publication Language: English

(30) Priority Data:

60/254,090 8 December 2000 (08.12.2000) US  
10/007,926 7 December 2001 (07.12.2001) US

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(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

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**Published:**

— without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS USING ARRAYS OF CANDIDATE GENES

(57) Abstract: The invention relates to a polynucleotide library useful in the molecular characterization of a carcinoma, the library including a pool of polynucleotide sequences of subsequences thereof wherein the sequences of subsequences are overpressed in tumor cells, further wherein the sequences of subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID NOS: 1-468 or the complement thereof. The invention relates also to polynucleotide arrays useful to differentiate tumor cells from normal cells comprising combinations of selected immobilized polynucleotide sequences sets.

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GENE EXPRESSION PROFILING OF PRIMARY BREAST  
CARCINOMAS USING ARRAYS OF CANDIDATE GENES

5 This invention relates to polynucleotide analysis  
and, in particular, to polynucleotide expression profiling of  
carcinomas using arrays of candidate polynucleotides.

10 Pathologists and clinicians in charge of the  
management of breast cancer patients are facing two major  
problems, namely the extensive heterogeneity of the disease  
and the lack of factors - among conventional histological and  
clinical features - predicting with reliability the evolution  
of the disease and its sensitivity to cancer therapies.  
Breast tumors of the same apparent prognostic type vary  
widely in their responsiveness to therapy and consequent  
15 survival of the patient. New prognostic and predictive  
factors are needed to allow an individualization of therapy  
for each patient.

20 Great hope is currently being placed on molecular  
studies, which address the problem in a global fashion.  
Methods such as cytogenetics, comparative genomic  
hybridization, and whole-genome allelotyping have addressed  
the issue at the genome level. Currently, the modifications  
that take place in human tumors at the level of transcription  
can also be studied in a large, unprecedented scale, using  
25 new methods such as cDNA arrays that allow quantitative  
measurement of the mRNA expression levels of many genes  
simultaneously. Thus, it would be advantageous to provide a  
means to assess the capacity of cDNA array testing in  
clinical practice to better classify an heterogeneous cancer  
30 into tumor subtypes with more homogeneous clinical outcomes,  
and to identify new potential prognostic factors and  
therapeutics targets.

The invention relates to a polynucleotide library useful in the molecular characterization of a carcinoma, the library including a pool of polynucleotide sequences or subsequences thereof wherein the sequences or subsequences are either underexpressed or overpressed in tumor cells, further wherein the sequences or subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 468 or the complement thereof.

Fig. 1 shows an example of differential gene expression between normal breast tissue (NB) and breast tumor samples.

Fig. 2 is a representation of expression levels of 176 genes in normal breast tissue (NB) and 34 samples of breast carcinoma.

Fig. 3 is prognostic classification of breast cancer by gene expression profiling.

Fig. 4 shows the correlation of GATA3 expression with ER phenotype.

In the context of this disclosure, a number of terms shall be utilized.

The term "polynucleotide" refers to a polymer of RNA or DNA that is single-stranded, optionally containing synthetic, non-natural or altered nucleotide bases. A polynucleotide in the form of a polymer of DNA may be comprised of one or more segments of cDNA, genomic DNA or synthetic DNA.

The term "subsequence" refers to a sequence of nucleic acids that comprises a part of a longer sequence of nucleic acids.

The term "immobilized on a support" means bound directly or indirectly thereto including attachment by

covalent binding, hydrogen bonding, ionic interaction, hydrophobic interaction or otherwise.

Breast cancer is characterized by an important histoclinical heterogeneity that currently hampers the selection of the most appropriate treatment for each case. This problem could be solved by the identification of new parameters that better predict the natural history of the disease and its sensitivity to treatment. An important object of the present invention relates to a large-scale molecular characterization of breast cancer that could help in prediction, prognosis and cancer treatment.

An important aspect of the invention relates to the use of cDNA arrays, which allows to quantitative study mRNA expression levels of 188 candidate genes in 34 consecutive primary breast carcinomas along three directions: comparison of tumor samples, correlations of molecular data with conventional histoclinical prognostic features and gene correlations. The experimentation evidenced extensive heterogeneity of breast tumors at the transcriptional level. Hierarchical clustering algorithm identified two molecularly distinct subgroups of tumors characterized by a different clinical outcome after chemotherapy. This outcome could not have been predicted by the commonly used histoclinical parameters. No correlation was found with the age of patients, tumor size, histological type and grade. However, expression of genes was differential in tumors with lymph node metastasis and according to the estrogen receptor status; ERBB2 expression was strongly correlated with the lymph node status ( $p \leq 0.0001$ ) and that of GATA3 with the presence of estrogen receptors ( $p \leq 0.001$ ). Thus, experimental results identified new ways to group tumors according to outcome and new potential targets of carcinogenesis. They show that the systematic use of cDNA



array testing holds great promise to improve the classification of breast cancer in terms of prognosis and chemosensitivity and to provide new potential therapeutic targets.

5 DNA arrays consist of large numbers of DNA molecules spotted in a systematic order on a solid support or substrate such as a nylon membrane, glass slide, glass beads or a silicon chip. Depending on the size of each DNA spot on the array, DNA arrays can be categorized as microarrays (each  
10 DNA spot has a diameter less than 250 microns) and macroarrays (spot diameter is greater than 300 microns). When the solid substrate used is small in size, arrays are also referred to as DNA chips. Depending on the spotting technique used, the number of spots on a glass microarray can  
15 range from hundreds to thousands.

DNA microarrays have serve a variety of purposes, including, gene expression profiling, de novo gene sequencing, gene mutation analysis, gene mapping and genotyping. cDNA microarrays are printed with distinct cDNA  
20 clones isolated from cDNA libraries. Therefore, each spot represents an expressed gene, since it is derived from a distinct mRNA.

Typically, a method of monitoring gene expression involves providing (1) providing a pool of sample  
25 polynucleotides comprising RNA transcript(s) of one or more target gene(s) or nucleic acids derived from the RNA transcript(s); (2) reacting, such as hybridizing the sample polynucleotide to an array of probes (for example, polynucleotides obtained from a polynucleotide library)  
30 (including control probes) and (3) detecting the reacted/hybridized polynucleotides. Detection can also involve calculating/quantifying a relative expression (transcription) level.

The present invention concerns a polynucleotide library useful in the molecular characterization of a carcinoma, said library comprising a pool of polynucleotide sequences or subsequences thereof wherein said sequences or subsequences are either underexpressed or overpressed in tumor cells, further wherein said sequences or subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID Nos: 1 - 468 in annex or the complement thereof.

Obviously, sequences having a great degree of homology with the above sequences could also been used to realize the molecular characterization of the invention, namely when those sequences present one or a few punctual mutations when compared with anyone of sequences SEQ ID Nos: 1 - 468.

The invention concerns a polynucleotide library useful in the molecular characterization of a carcinoma, said library comprising a pool of polynucleotide sequences or subsequences thereof wherein said sequences or subsequences are overpressed in tumor cells, further wherein said sequences or subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 249 (Here, these SEQ ID N° refer to old SEQ ID N° 1-249 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex ) or the complement thereof

Preferably the pool of polynucleotide sequences or subsequences correspond substantially to the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 247 (Here, these SEQ ID N° refer to old SEQ ID N° 1-247 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application

in annex); further wherein said sequences are useful in differentiating a normal cell from a cancer cell.

5 The invention relates also to a polynucleotide library wherein the pool of polynucleotide sequences or subsequences correspond substantially to the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 242 (Here, these SEQ ID N° refer to old SEQ ID N° 1-242 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex);  
10 wherein said sequences are useful in detecting a hormone sensitive tumor cell, or wherein said sequences are useful in differentiating a tumor with lymph nodes from a tumor without lymph nodes.

15 The invention relates also to a polynucleotide library wherein the pool of polynucleotide sequences or subsequences correspond substantially to the polynucleotide sequences set forth in any of SEQ ID NOS: 1 - 224; (Here, these SEQ ID N° refer to old SEQ ID N° 1-224 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex) wherein said sequences are useful in differentiating tetracycline-sensitive tumors from tetracycline-insensitive tumors.

20 The invention relates also to any polynucleotide library as previously described wherein said polynucleotides are immobilized on a solid support in order to form a polynucleotide array.

25 Preferably the support is selected from the group consisting of a nylon membrane, glass slide, glass beads, or a silicon chip.

The invention concerns also a method for detecting differentially expressed polynucleotide sequences which are correlated with a cancer, said method comprising:

- a) obtaining a polynucleotide sample from a patient; and
- 5        b) reacting the sample polynucleotide obtained in step (a) with a probe immobilized on a solid support wherein said probe comprises any of the polynucleotide sequences of the libraries previously described or an expression product encoded by any of the polynucleotide sequences of said
- 10       libraries and
- c) detecting the reaction product of step (b).

The invention relates also to a such method for detecting differentially expressed polynucleotide sequences

15       of the invention wherein the amount of reaction product of step (c) is compared to a control sample.

Preferably the polynucleotide sample isolated for, the sample is RNA or mRNA.

Preferably the polynucleotide sample is cDNA obtained by

20       reverse transcription of the mRNA.

In a preferred embodiment the method for detecting differentially expressed polynucleotide sequences, the step (b) comprises a hybridization of the sample RNA with the labeled probe.

25       The method for detecting differentially expressed polynucleotide sequences is used for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating conditions associated with cancer, and namely breast cancer.

30       The method for detecting differentially expressed polynucleotide sequences is particularly useful wherein the product encoded by any of the polynucleotide sequences or

subsequences is involved in a receptor-ligand reaction on which detection is based.

The invention relates also to a method for screening an anti-tumor agent comprising the method for detecting differentially expressed polynucleotide sequences previously described wherein the sample has been treated with the anti-tumor agent to be screened.

The label used to label polynucleotide samples is selected from the group consisting of radioactive, colorimetric, enzymatic, molecular amplification, bioluminescent or fluorescent label.

The invention also relates to a library of polynucleotides comprising a population of polynucleotide sequences overexpressed or underexpresses in cells derived from a tumor selected from SEQ ID NO :1 to SEQ ID NO :249 and their respective complements. (Here, these SEQ ID N° refer to old SEQ ID N° 1-249 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex).

In a particular embodiment the invention relates to polynucleotide sequences: SEQ ID No : 1 ; SEQ ID No : 5 ; SEQ ID No : 8 ; SEQ ID No : 9 ; SEQ ID No : 28 ; SEQ ID No : 29 ; SEQ ID No : 30 ; SEQ ID No : 31 ; SEQ ID No : 32 ; SEQ ID No : 45 ; SEQ ID No : 46 ; SEQ ID No : 52 ; SEQ ID No : 54 ; SEQ ID No : 63 ; SEQ ID No : 64 ; SEQ ID No : 81 ; SEQ ID No : 82 ; SEQ ID No : 87 ; SEQ ID No : 88 ; SEQ ID No : 101 ; SEQ ID No : 102 ; SEQ ID No : 103 ; SEQ ID No : 104 ; SEQ ID No : 105 ; SEQ ID No : 107 ; SEQ ID No : 113 ; SEQ ID No : 114 ; SEQ ID No : 115 ; SEQ ID No : 116 ; SEQ ID No : 127 ; SEQ ID No : 128 ; SEQ ID No : 131 ; SEQ ID No : 139 ; SEQ ID No : 140 ; SEQ ID No : 142 ; SEQ ID No : 150 ; SEQ ID No : 151 ; SEQ ID No : 154 ; SEQ ID No : 156 ; SEQ ID

No : 160 ; SEQ ID No : 161 ; SEQ ID No : 162 ; SEQ ID No : 177 ;  
SEQ ID No : 178 ; SEQ ID No : 194 ; SEQ ID No : 195 ; SEQ ID No :  
227 ; SEQ ID No : 228 ; SEQ ID No : 229 ; SEQ ID No : 231 ; SEQ ID  
No : 233 ; SEQ ID No : 243 ; SEQ ID No : 244 ; SEQ ID No : 245 ;  
5 SEQ ID No : 246 ; SEQ ID No : 247, (Here, these SEQ ID N° refer  
to old SEQ ID N° presented on table 5 in priority document,  
the correlation table 10 allows to identify these sequences  
in the sequence listing of the present application in annex),  
which distinguish a healthy person from a person with cancer.

10 Preferably the invention relates to  
polynucleotide sequences: SEQ ID No : 1 ; SEQ ID No : 5 ; SEQ ID  
No : 102 ; SEQ ID No : 103 ; SEQ ID No : 107 ; SEQ ID No : 229 ;  
SEQ ID No : 45 ; SEQ ID No : 46 ; SEQ ID No : 243 ; SEQ ID No :  
244 ; SEQ ID No : 245 ; SEQ ID No : 246 ; SEQ ID No : 247 (Here,  
15 these SEQ ID N° refer to old SEQ ID N° presented on table 6  
in priority document, the correlation table 10 allows to  
identify these sequences in the sequence listing of the  
present application in annex), which distinguish a healthy  
person from a person with cancer.

20 In another particular embodiment the invention relates  
to polynucleotide sequences: SEQ ID No : 2 ; SEQ ID No : 3 ;  
SEQ ID No : 4 ; SEQ ID No : 5 ; SEQ ID No : 6 ; SEQ ID No : 7 ;  
SEQ ID No : 8 ; SEQ ID No : 9 ; SEQ ID No : 10 ; SEQ ID No : 11 ;  
25 SEQ ID No : 12 ; SEQ ID No : 13 ; SEQ ID No : 14 ; SEQ ID No : 15  
; SEQ ID No : 16 ; SEQ ID No : 17 ; SEQ ID No : 18 ; SEQ ID No :  
19 ; SEQ ID No : 20 ; SEQ ID No : 21 ; SEQ ID No : 22 ; SEQ ID No  
: 23 ; ; SEQ ID No : 24 ; SEQ ID No : 25 ; SEQ ID No : 26 ; SEQ ID  
No : 27 ; SEQ ID No : 221 ; SEQ ID No : 222 ; SEQ ID No : 223 ;  
30 SEQ ID No : 241 ; SEQ ID No : 242 (Here, these SEQ ID N° refer  
to old SEQ ID N° presented on table 7 in priority document,  
the correlation table 10 allows to identify these sequences  
in the sequence listing of the present application in annex)  
which detect hormone sensitive tumors.

Preferably the invention relates to polynucleotide sequences SEQ ID No : 1; SEQ ID No : 2 SEQ ID No : 3; SEQ ID No : 4; SEQ ID No : 5; SEQ ID No : 221; SEQ ID No : 222 ; SEQ ID No : 15; SEQ ID No : 16; SEQ ID No : 17; SEQ ID No : 18 ; SEQ ID No : 19; SEQ ID No : 20 ; SEQ ID No : 21; SEQ ID No : 22 ; SEQ ID No : 241; SEQ ID No : 242 (Here, these SEQ ID N° refer to old SEQ ID N° presented on table 8 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex), which detect hormone sensitive tumors.

In another particular embodiment the invention relates to polynucleotide sequences: SEQ ID No : 1 ; SEQ ID No : 3 ; SEQ ID No : 4 ; SEQ ID No : 19 ; SEQ ID No : 20 ; SEQ ID No : 21; SEQ ID No : 22 ; SEQ ID No : 23 ; SEQ ID No : 26 ; SEQ ID No : 27 ; SEQ ID No : 28 ; SEQ ID No : 29 ; SEQ ID No : 30 ; SEQ ID No : 31 ; SEQ ID No : 32 ; SEQ ID No : 33 ; SEQ ID No : 34 ; SEQ ID No : 35 ; SEQ ID No : 36; SEQ ID No : 37; SEQ ID No : 38; SEQ ID No : 39; SEQ ID No : 40 ; SEQ ID No : 41 ; SEQ ID No : 42 ; SEQ ID No : 43 ; SEQ ID No : 44 ; SEQ ID No : 221 ; SEQ ID No : 222 ; SEQ ID No : 233 ; SEQ ID No : 241 ; SEQ ID No : 242 (Here, these SEQ ID N° refer to old SEQ ID N° presented on table 8 in priority document, the correlation table 10 allows to identify these sequences in the sequence listing of the present application in annex), which distinguish tumors with lymph node from tumors with no lymph node.

Preferably the invention relates to polynucleotide sequences : SEQ ID No : 1 ; SEQ ID No : 21 ; SEQ ID No : 22 ; SEQ ID No : 28; ; SEQ ID No : 29 ; SEQ ID No : 29 ; SEQ ID No : 31 ; SEQ ID No : 32 ; SEQ ID No : 19 ; SEQ ID No : 20 ; SEQ ID No : 26 ; SEQ ID No : 27 ; SEQ ID No : 37 ; SEQ ID No : 38 ; SEQ ID No : 39 ; SEQ ID No : 241 ; SEQ ID No : 241, (Here, these SEQ ID N° refer to old SEQ ID N° presented on table 8 in priority document, the correlation table 10 allows to

identify these sequences in the sequence listing of the present application in annex), which distinguish tumors with lymph node from tumors with no lymph node.

5           In another particular embodiment the invention relates to polynucleotide sequences: SEQ ID No : 1 ; SEQ ID No : 2 ;  
SEQ ID No : 6 ; SEQ ID No : 7 ; SEQ ID No : 8 ; SEQ ID No : 9 ;  
10       SEQ ID No : 10 ; SEQ ID No : 11 ; SEQ ID No : 13 ; SEQ ID No : 14 ;  
SEQ ID No : 19 ; SEQ ID No : 20 ; SEQ ID No : 21 ; SEQ ID No :  
22 ; SEQ ID No : 23 ; SEQ ID No : 35 ; SEQ ID No : 36 ; ; SEQ ID  
15       No : 37 ; SEQ ID No : 56 ; SEQ ID No : 57 ; SEQ ID No : 74 ; SEQ  
ID No : 75 ; SEQ ID No : 102 ; SEQ ID No : 104 ; SEQ ID No : 107  
; SEQ ID No : 108 ; SEQ ID No : 109 ; SEQ ID No : 118 ; SEQ ID No  
: 119 ; ; SEQ ID No : 136 ; SEQ ID No : 213 ; SEQ ID No : 214 ;  
20       SEQ ID No : 215 ; SEQ ID No : 223 ; SEQ ID No : 224 (Here, these  
SEQ ID N° refer to old SEQ ID N° presented on table 11 in  
priority document, the correlation table 10 allows to  
identify these sequences in the sequence listing of the  
present application in annex) which distinguish tumors  
sensitive to anthracycline from tumors unsensitive to  
anthracycline.

25           The invention relates also to a method of detecting differentially expressed genes correlated with a cancer comprising detecting at least one library of polynucleotide sequences as above defined or of products encoded by said library in a sample obtained from a patient.

30           A particular embodiment of the invention relates to a polynucleotide library of corresponding substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets 1 to set 212 as defined in table 4



The invention relates obviously to polynucleotide libraries comprising at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of said predefined sets, allowing to obtain a discriminating gene pattern, namely to distinguish between normal patients and patients suffering from tumor pathology, between patients having an hormone sensitive tumor and patients having an hormone resistant tumor, between patients having a tumor with lymph nodes from patients having a tumor without lymph nodes, between patients having an antracycline-sensitive tumor from patients having an antracycline-insensitive tumor and between patients having good prognosis primary breast tumors and patients having poor prognosis primary breast tumors.

Polynucleotide sequences library useful for the realization of the invention can comprise also any sequence comprised between 3'end and 5'end of each polynucleotide sequence set as defined in table 4, allowing the complete detection of the implicated genes.

The invention relates also to a polynucleotide library useful to differentiate a normal cell from a cancer cell wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets indicated on table 5, useful in differentiating a normal cell from a cancer cell.

Preferably the polynucleotide library useful to differentiate a normal cell from a cancer cell correspond

substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets indicated on table 5A, and of at least one polynucleotide sequence  
5 selected among those included in each one of predefined polynucleotide sequences sets indicated in table 5B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 5A, together with detection of an underexpression of  
10 genes identified with sets of polynucleotides sequences defined in table 5B allows to distinguish between normal patients, and patients suffering from tumor pathology.

The invention relates also to a polynucleotide library useful to detect a hormone sensitive tumor cell  
15 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in  
20 table 6

Preferably the polynucleotide library useful to detect a hormone sensitive tumor cell correspond substantially to any combination of at least one  
25 polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6B.

30 The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 6A, together with detection of an underexpression of

genes identified with sets of polynucleotides sequences defined in table 6B allows to distinguish between patients having an hormone sensitive tumor and patients having an hormone resistant tumor.

5

The invention concerns also a polynucleotide library useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7.

Preferably, the polynucleotide library useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 7A, together with detection of an underexpression of genes identified with sets of polynucleotides sequences defined in table 7B allows to distinguish between patients having a tumor with lymph nodes from patients having a tumor without lymph nodes.

The invention concerns also a polynucleotide library useful to differentiate anthracycline-sensitive tumors

from antracycline-insensitive tumors wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8.

Preferably, the polynucleotide library useful to differentiate antracycline-sensitive tumors from antracycline-insensitive tumors correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 8A, together with detection of an underexpression of genes identified with sets of polynucleotides sequences defined in table 8B allows to distinguish between patients having an antracycline-sensitive tumor from patients having an antracycline-insensitive tumor.

The invention concerns also a polynucleotide library useful to classify good and poor prognosis primary breast tumors wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9.

Preferably, the polynucleotide library useful to classify good and poor prognosis primary breast tumors correspond substantially to any combination of at least one

polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9B.

The detection of an overexpression of genes identified with sets of polynucleotides sequences defined on table 9A, together with detection of an underexpression of genes identified with sets of polynucleotides sequences defined in table 9B allows to classify patients having good and poor prognosis primary breast tumors.

In a preferred embodiment, the tumor cell presenting underexpressed or overpressed sequences from the polynucleotide library of the invention are breast tumor cells.

In a particular embodiment the polynucleotides of the polynucleotide library of the present invention are immobilized on a solid support in order to form a polynucleotide array, and said solid support is selected from the group consisting of a nylon membrane, nitrocellulose membrane, glass slide, glass beads, membranes on glass support or a silicon chip.

Another object of the present invention concerns a polynucleotide array useful for prognosis or diagnostic of tumor comprising at least one immobilized polynucleotide library set as previously defined.

Then the invention concerns a polynucleotide array useful to differentiate a normal cell from a cancer cell comprising any combination of at least one polynucleotide sequence selected among those included in each

one of predefined polynucleotide sequences sets indicated on table 5, useful in differentiating a normal cell from a cancer cell.

5 Preferably the polynucleotide array useful to differentiate a normal cell from a cancer cell bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets indicated on table 5A, and of at least one polynucleotide sequence selected among those included in each  
10 one of predefined polynucleotide sequences sets indicated in table 5B.

The invention relates also to a polynucleotide array useful to detect a hormone sensitive tumor cell  
15 comprising any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6

20 Preferably the polynucleotide array useful to detect a hormone sensitive tumor cell bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 6A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in  
25 table 6B.

30 The invention concerns also a polynucleotide array useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes comprising any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7.

Preferably, the polynucleotide array useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 7B.

The invention concerns also a polynucleotide array useful to differentiate anthracycline-sensitive tumors from anthracycline-insensitive tumors comprising any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8.

Preferably, the polynucleotide array useful to differentiate anthracycline-sensitive tumors from anthracycline-insensitive tumors bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 8B.

The invention concerns also a polynucleotide array useful to classify good and poor prognosis primary breast tumors comprising any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9.

Preferably, the polynucleotide array useful to classify good and poor prognosis primary breast tumors bears any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9A together with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets defined in table 9B.

The present invention concerns also a method for detecting differentially expressed polynucleotide sequences that are correlated with a cancer, said method comprising:

a) obtaining a polynucleotide sample from a patient; and

b) reacting the sample polynucleotide obtained in step (a) with a probe immobilized on a solid support wherein said probe comprises any of the polynucleotide sequences of the libraries previously defined or an expression product encoded by any of the polynucleotide sequences of the libraries previously defined

c) detecting the reaction product of step (b).

Preferably, the polynucleotide sample obtained at step (a) is labeled before its reaction at step (b) with the probe immobilized on a solid support.

The label of the polynucleotide sample is selected from the group consisting of radioactive, colorimetric, enzymatic, molecular amplification, bioluminescent or fluorescent.



In a particular embodiment the reaction product of step (c) is quantified by further comparison of said reaction product to a control sample.

In a first embodiment, the polynucleotide sample isolated from the patient and obtained at step (a) is either RNA or mRNA.

In another embodiment the polynucleotide sample isolated from the patient is cDNA is obtained by reverse transcription of the mRNA.

Preferably the reaction step (b) of the method for detecting differentially expressed polynucleotide sequences comprises a hybridization of the sample RNA issued from patient with the probe.

Preferably the sample RNA is labeled before hybridization with the probe and the label is selected from the group consisting of radioactive, colorimetric, enzymatic, molecular amplification, bioluminescent or fluorescent.

This method for detecting differentially expressed polynucleotide sequences is particularly useful for detecting, diagnosing, staging, monitoring, prognosticating, preventing or treating conditions associated with cancer, and particularly breast cancer.

The method for detecting differentially expressed polynucleotide sequences is also particularly useful when the product encoded by any of the polynucleotide sequences or subsequences set is involved in a receptor-ligand reaction on which detection is based.

The present invention is also related with a method for screening an anti-tumor agent comprising the method the above-depicted method for detecting differentially expressed polynucleotide sequences wherein the sample has been treated with the anti-tumor agent to be screened.

In a particular embodiment the method for screening an anti-tumor agent comprises detecting polynucleotide sequences reacting with at least one library of polynucleotides or polynucleotide sequences set as previously defined or of products encoded by said library in a sample obtained from a patient.

The invention is illustrated by examples detailed below related to particular experimental results obtained with selected libraries of polypeptides useful to identify and distinguish tumor samples from normal ones.

#### Tumor samples and RNA extraction

To avoid any bias of selection as to the type and size of the tumors, the RNAs to be tested were prepared from unselected samples. Samples of primary invasive breast carcinomas were collected from 34 patients undergoing surgery at the Institute Paoli-Calmette. After surgical resection, the tumors were macrodissected: a section was taken for the pathologist's diagnosis and an adjacent piece was quickly frozen in liquid nitrogen for molecular analyses. The median age of patients at the time of diagnosis was 55 years (range 39, 83) and most of them were post-menopausal. Tumors were classified according to the WHO histological typing of breast tumors in: 29 ductal carcinomas, 2 lobular carcinomas, 1 mixed ductal and lobular carcinoma, and 2 medullar carcinomas. They had various sizes, inferior or equal to 20 mm (n = 13), between 20 and 50 mm (n = 18) or superior to 50 mm (n = 3), axillary's lymph node status (negative: 19 tumors, positive: 15 tumors), SBR grading (I: 3 tumors, II: 20 tumors, III: 10 tumors, not evaluable: 1 tumor), and estrogen receptor status (ER) evaluated by

immunohistochemical assay (23 ER-positive, 11 ER-negative). ER positivity cutoff value was 10%. Adjuvant treatment with radiotherapy and when necessary multi-agent anthracyclin-based chemotherapy (n = 16) was given to patients according to local practice.

Total RNA was extracted from tumor samples by standard methods (43). Total RNA from normal breast tissue was obtained from Clontech (Palo Alto, CA): RNA was isolated from 8 tissue specimens from Caucasian females, age range 23 - 47. RNA integrity was controlled by denaturing formaldehyde agarose gel electrophoresis and Northern blots using a 28S-specific oligonucleotide.

#### cDNA arrays preparation

Gene expression was analyzed by hybridization of arrays with radioactive probes. The arrays contained PCR products of 5 control clones, and 180 IMAGE human cDNA clones selected with practical criteria (3' sequence of mRNA, same cloning vector, host bacteria and insert size). This represented 176 genes (4 genes were represented by 2 different clones): 121 with proven or putative implication in cancer and 55 implicated in immune reactions (the list is available on the web site: <http://tagc.univ-mrs.fr/pub/Cancer/>). Their identity was verified by 5' tag-sequencing of plasmid DNA and comparison with sequences in the EST (dbEST) and nucleotide (GenBank) databases at the NCBI. Identity was confirmed for all but 14 clones without significant gene similarity, which were referenced by their GenBank accession number. The control clones were: Arabidopsis thaliana cytochrome c554 gene (used for hybridization signal normalization), 3 poly(A) sequences of different sizes and the vector pT7T3D (negative controls).

PCR amplification, purification and robotical spotting of PCR products onto Hybond-N+ membranes (Amersham) were done according to described protocols (4). All PCR products were spotted in duplicate. For normalization purpose, the c554 gene was spotted 96-fold scattered over the whole membrane.

#### cDNA array hybridizations

Hybridizations were done successively with a vector oligonucleotide (to precisely determine the amount of target DNA accessible to hybridization in each spot), then after stripping of vector probe, with complex probes made from the RNAs (4). Each complex probe was hybridized to a distinct filter. Probes were prepared from total RNA with an excess of oligo(dT25) to saturate the poly(A) tails of the messengers, and to insure that the reverse transcribed product did not contain long poly(T) sequences. A precise amount of c554 mRNA was added to the total RNA before labeling to allow normalization of the data.

Five ng of total RNA (~100ng of mRNA) from tissue samples were used for each labeling. Probe preparation and hybridization of the membranes were done according to known procedures (<http://tagc.univ-mrs.fr/pub/Cancer/>).

Hybridization was done in excess of target (~15 ng of DNA in each spot) and binding of cDNAs to the targets was linear and proportional to the quantity of cDNA in the probe.

#### Detection and quantification of cDNA array hybridization signals

Quantitative data were obtained using an imaging plate device. Hybridization signal detection with a FUJI BAS 1500 machine and quantification with the HDG Analyzer

software (Genomic Solutions, Ann Arbor, MI) were done as previously described (<http://tagc.univ-mrs.fr/pub/Cancer/>). Quantification was done by integrating all spot pixel intensities and subtracting a spot background value determined in the neighboring area. Spots were located with a LaPlacian transformation. Spot background level was the median intensity of all the pixels present in a small window centered on the spot and which were not part of any spot (44). Quantified data were normalized in three steps and expressed as absolute gene expression levels (i.e. in percentage of abundance of individual mRNA with respect to mRNA within the sample), as described (4).

#### Array data analysis

Before analysis of the results, the reproducibility of the experiments was verified by comparing duplicate spots, or one hybridization with the same probe on two independent arrays, or two independent hybridizations with probes prepared from the same RNA. In every case, the results showed good reproducibility with respective correlation coefficients of 0.95, 0.98 and 0.98 (data not shown). Moreover, genes represented by two different clones on the array, such as CDK4 or ETV5, displayed similar expression profiles for the two clones in all samples. This reproducibility was sufficient enough to consider a 2-fold expression difference as significantly differential.

For graphical representation, data were displayed as absolute expression levels (Fig. 2a). For better visualization of clustering, results were log-transformed and displayed as relative values median-centered in each row and in each column (Fig. 2b). Hierarchical clustering was applied to the tissue samples and the genes using the Cluster program developed by Eisen (45) (average linkage clustering

using Pearson correlation as similarity metric). Results in Figs. 2 and 3 were displayed with the TreeView program (45).

Subsequent analysis was done using Excel software (Microsoft) and statistical analyses with the SPSS software. Metastasis-free survival and overall survival were measured from diagnosis until the first metastatic relapse or death respectively. They were estimated with the Kaplan-Meier method and compared between groups with the Log-Rank test. Correlations of gene pairs based on expression profiles were measured with the correlation coefficient  $r$ . The search for genes with expression levels correlated with tumor parameters was done in several successive steps.

First, genes were detected by comparing their median expression level in the two subgroups of tumors discordant according to the parameter of interest. The median values rather than the mean values were used because of the high variability of the expression levels for many genes, resulting in a standard deviation of expression level similar or superior to the mean value and making comparisons with means impossible. Second, these detected genes were inspected visually on graphics, and finally, an appropriate statistical analysis was applied to those that were convincing to validate the correlation. Comparison of GATA3 expression between ER-positive tumors and ER-negative tumors was validated using a Mann-Witney test. Correlation coefficients were used to compare the gene expression levels to the number of axillary nodes involved.

#### Northern blot analysis

Seventy-nine breast tumors, including 22 of the 34 tested on the arrays, were analyzed for GATA3 expression by Northern blot hybridization. RNA extraction from tumor samples and Northern blots were done as previously described

(43). The GATA3 probe was prepared from the IMAGE cDNA clone 129757, which corresponds to the 3' region (from +843 to +1689) of the GATA3 cDNA sequence (GenBank accession no. X55122). The insert (846 bp) was obtained by digestion of the clone with EcoRI and PacI enzymes. Northern blots were stripped and re-hybridized using a  $\alpha$ -actin probe (46).

Fig. 1 shows an example of differential gene expression between normal breast tissue (NB) and breast tumor samples. Each cDNA array on Nylon filter was hybridized with a complex probe made from 5  $\mu$ g of total RNA. The top image corresponds to the whole membrane. For the two bottom images, only the right portion of the membranes is shown. Numbers below the spots indicate housekeeping genes (1, GAPDH and 2, actin), negative control clones (3, 4 and 5) and examples of genes differentially expressed between NB and breast tumor (6, stromelysin3; 7, ERBB2; 8, MYBL2; 9, FOS; 10, TGF $\beta$ 3; 11, desmin), and between ER- breast tumor and ER+ breast tumor (12, GATA3).

Fig. 2 is a representation of expression levels of 176 genes in normal breast tissue (NB) and 34 samples of breast carcinoma. Each column corresponds to a single tissue, and each row to a single gene. (a) The results are expressed as percentage abundance of individual mRNA within the sample, and are represented using a blue color scale. The color scale (log scale with a 3-fold interval) indicated at the bottom left ranges from light blue (expression level 0.001%) to dark blue (expression level > 3%). White squares indicate clones with undetectable expression levels and gray squares indicate missing data. The tissue samples are arbitrarily ordered and the clones are ordered from top to bottom according to increasing median expression levels. Horizontal black arrows on the right of the figure mark three clones with highly variable expression levels between the

tumors (stromelysin3, IGF2, GATA3 from top to bottom). (b) The results are shown as relative expression levels (relative to the median value of each row and each column) and are represented with a color scale indicated at the bottom left ranging from 1/100 to 100 fold changes (gray squares: missing data). Eighteen clones with median expression level equal to zero in the 34 tumors are omitted. The clustering program arranges samples (n = 35) along the horizontal axis so that those with the most similar expression profiles are placed adjacent to each other. Similarly, clones (n = 162) are near each other along the vertical axis if they show a strong expression profile correlation across all tissues. The length of the branches of the dendrograms capturing respectively the samples (top) and the clones (left) reflects the similarity of the related elements. Two groups of tumors are separated and color coded: group A (blue) and group B (orange). Horizontal black and horizontal red arrows on the right of the figure respectively mark three genes with highly variable expression levels between the tumors (IGF2, GATA3, stromelysin3 from top to bottom) and four pairs of different clones representing four genes. (c) Zoom representation of group A from Figure 2b, excluding the two outlier tumors at the right. The clustering separates two subgroups of tumors, A1 and A2. The dotted branches correspond to tumors associated with metastatic relapse and death. Follow-up was longer in A2 than in A1 (median 81 months vs 47 for A1).

Fig. 3 is prognostic classification of breast cancer by gene expression profiling showing that gene expression-based tumour classification correlates with clinical outcome. The 12 samples of group A (see figure 2b and 2c) were reclustered using the top 32 differentially expressed genes between A1 and A2 subgroups. Data were displayed as in Fig. 2b and shown with the same color key.



The hierarchical clustering was applied to expression data from the 23 clones, out of 32, of which expression levels presented an at least two-fold change in at least two samples (out of 12). Two subgroups of tumors A1 and A2 are shown as well as two groups of differentially expressed clones. The dotted branches of tumor cluster A1 correspond to samples associated with metastatic relapse and death. Figure 3a shows Two-dimensional representation of hierarchical clustering results shown in figures 2a and 2b. The analysis delineates 4 groups of tumours A, B, C and D. Black squares indicate patients alive at last follow-up visit and red squares indicate patients who died. Three classes of patients with a statistically different clinical outcome were defined according to gene expression profiles: class A (n = 16), class B+C (n = 34), class D (n = 5). Figure 3b illustrates Kaplan-Meier plot of overall survival of the 3 classes of patients ( $p < 0.005$ , log-rank test). And figure 3c illustrates Kaplan-Meier plot of metastasis-free survival of the 3 classes of patients ( $p < 0.05$ , log-rank test).

Fig. 4 shows the correlation of GATA3 expression with ER phenotype. (a) The expression levels of GATA3 in 34 breast cancer samples (y axis) monitored by cDNA array analysis are reported in percentage of abundance of individual mRNA with respect to mRNA within the sample (log scale). GATA3 is significantly overexpressed in the ER-positive tumors (n = 23) versus the ER-negative tumors (n = 11) using the Mann-Witney test ( $p = 0.0004$ ). The expression level of GATA3 in normal breast tissue is reported on the right (NB). (b) Northern blot analysis of GATA3 in normal breast sample (NB) and 9 breast cancer samples (AT: tumor analyzed with cDNA array and Northern blot; NT: tumor analyzed with Northern blot). Blots were probed successively

with cDNA from GATA3 (top) and  $\alpha$ -actin (bottom). ER status is indicated for each tumor sample.

#### Data representation

5 Fig. 1 shows examples of hybridizations of cDNA arrays with probes made from RNA extracted from normal breast tissue and breast tumors.

10 The crude results of all hybridizations were processed to be presented either as absolute or relative values in schematic figures. The normalization procedure allowed display of absolute values expressed in percent of abundance of mRNA in the probe as shown in Fig. 2a. Each level of the blue color ladder represents a 3-fold interval of absolute abundance of mRNA. Each column corresponds to a tissue sample and each row to a gene. For graphic purposes, genes were ordered from top to bottom according to increasing median expression levels. Tumor samples were not ordered. The values in each sample displayed a wide range of intensities (3 decades in log scale) corresponding to expression levels ranging from approximately 0.002% to 5% of mRNA abundance. Many genes (see for example stromelysin 3, IGF2 and GATA3, arrows) displayed highly variable expression levels across all tumor samples, scattered over the whole dynamic range of values. A representation of relative values is shown in Fig. 2b. Absolute values were log-transformed, omitting 18 clones whose median intensity was equal to zero across all tissues. Data for each of the 162 remaining clones were then median-centered, as well as data for each sample, so that the relative variation was shown, rather than the absolute intensity. A color scale was used to display data: red for expression level higher than the median and green for expression level lower than the median. The magnitude of the deviation from the median was represented by

15

20

25

30

the color intensity. A hierarchical clustering program was then applied to group the 35 samples according to their overall gene expression profiles, and to group the 162 clones on the basis of similarity of their expression levels in all tissues. This resulted in a picture highlighting groups of correlated tissues and groups of correlated genes as depicted by dendrograms.

#### Breast tumor classification

As shown in Fig. 2b, the clustering algorithm identified two groups of samples, designated A ( $n = 15$ , including normal breast, NB) and B ( $n = 20$ ). These groups were similar with respect to patient age, menopausal status at diagnosis, SBR grading and tumor pathological size. However, 72% of tumors in group A were node-positive and 75% in group B were node-negative. Moreover, 80% of the tumors in group B were estrogen receptor (ER) positive and 50% in group A were ER-negative. With a median follow-up of 44 months after diagnosis, overall survival was different between A and B groups: 5 women died in A (median follow-up 58 months) and 1 in B (median follow-up 40 months). But the frequency of metastatic relapse was relatively similar in the two groups, with 5 women who relapsed in A and 6 in B. Because the time between the diagnosis of metastasis and last follow-up is too short in B, a longer follow-up is needed to determine if these two different groups, defined with expression profiles, have really a different outcome with respect to overall survival.

In the group A of 15 samples, three samples (normal breast and two tumors) were different from each other and from the other 12 samples. The latter constituted two subgroups of tumors, A1 ( $n = 6$ ) and A2 ( $n = 6$ ), which could be further separated by clustering as shown in Fig. 2c. The

12 tumors had an uniformly high risk of metastatic relapse according to conventional prognostic features as shown in Table 1. Most of them had received comparable adjuvant anthracyclin-based chemotherapy after surgery, with more women treated in the A1 subgroup. Interestingly, these two subgroups, which could not be distinguished with commonly used histoclinical features, had a very different clinical outcome: there were 4 metastatic relapses and 4 deaths in A1 (median follow-up: 44 months). In contrast and despite a longer median follow-up (90 months), no metastasis or death occurred in A2. This resulted in a significant better metastasis-free survival ( $p = 0.01$ ) and overall survival ( $p = 0.005$ ) for group A2 than for group A1 tumors. No such subgrouping could be done in B.

TABLE 1

Subgroup	A1						A2					
Tumor position in the cluster	1	2	3	4	5	6	7	8	9	10	11	12
Age, years	46	58	60	63	51	58	46	47	50	47	46	66
Nodal status	1	0	0	16	13	37	10	4	1	2	0	0
Histological size, mm	60	20	26	35	20	30	27	25	30	25	20	22
SBR grade												
ER status	neg	neg	neg	neg	neg	neg	pos	neg	pos	pos	pos	pos
Adjuvant chemotherapy	yes	yes	no	yes	yes	yes	yes	yes	no	yes	no	no
Metastasis	yes	no	yes	yes	no	yes	no	no	no	no	no	no
Follow-up, months	58	106	35	47	41	31	85	98	95	49	19	141
Patient status	D	A	D	D	A	D	A	A	A	A	A	A

Patient characteristics in subgroups A1 and A2. The 12 tumors are numbered from 1 to 12 according to their position from left to right in the clustering graphic displayed in Fig. 3. Adjuvant chemotherapy was anthracyclin-based. In the line concerning the patient status, A means alive and D means death from cancer progression.

Genes responsible for group A substructure were searched. These are potentially relevant to the prognosis and the sensitivity to chemotherapy in these tumors. Thirty-two genes out of 188 were identified by comparing their median expression level in A1 vs A2. Then, the 12 tumors were reclustered using the expression profiles of these genes as shown in Fig. 3. The same subgroups A1 and A2 were evident and separated by 2 groups of genes: as expected, high expression of ERBB2, MYC and EGFR was associated with bad prognosis subgroup A1 (6-8), and that of E-cadherin and the proto-oncogene MYB with good prognosis subgroup A2 (9, 10). For most of the other genes, these results may stimulate new investigations. Differentiation state is a good prognostic factor in breast cancer and, accordingly, genes associated with cell differentiation, such as GATA3 (11) and CRABP2 (12), had a high level of expression in the better outcome group. The high expression of Ephrin-A1 mRNA in the bad prognosis subgroup suggests a role of this growth factor in breast cancer and can be paralleled with its up-regulation during melanoma progression (13).

Differential gene expression between normal breast and breast tumors

To identify genes differentially expressed between breast tumors (T) and normal breast (NB), the NB value for each gene was compared to its expression level in each tumor. When the expression level of a gene in NB was undetectable, only qualitative information could be deduced and the mRNA was considered as differentially expressed if the signal intensity in the tumor was superior to the reproducibility threshold (0.002% of mRNA abundance). In the other cases, differential expression was defined by an at least 2-fold expression difference. Also, the number of

tumors where it was over- or underexpressed was measured. Table 2 shows a list of the top 20 over- and underexpressed genes. For these genes, the T/NB ratio is reported, where T represented their median expression value in the 34 tumors. This ratio ranged from 2.70 (ABCC5) to 17.76 (GATA3) for the overexpressed genes, and from 0.00 (desmin) to 0.29 (APC) for the underexpressed genes.

**TABLE 2**

Clone ID	Gene/Protein identity	Gene symbol	Chrom. location	N	T/NB
	Overexpressed genes				
154343	Granzyme H	GZMH	14q11.2	32	9,51
235947	Stromelysin 3	STMY3	22q11.2	31	15,92
207378	MYB Related Protein B	MYBL2	20q13.1	31	(a)
153275	Cellular Retinoic Acid Binding Protein 2	CRABP2	1q21.3	29	7,16
129757	GATA-binding protein 3	GATA3	10p15	28	17,76
120649	T-Lymphocyte surface CD2 antigen	CD2	1p13.1	28	7,54
109677	CREB Binding Protein	CREBBP	16p13.3	28	5,08
172152	EGFR-binding protein GRB2	GRB2	17q24-q25	28	5,00
66969	Transcription factor RELB	RELB	19	28	3,61
182007	ETS-Related Transcription Factor ELF1	ELF1	13q13	27	3,58
153446	LIM domain protein RIL	RIL	5q31.1	26	4,03
203394	ETS Variant gene 5 (ETS-related molecule)	ETV5	3q28	25	3,67
160963	Thrombospondin 1	THBS1	15q15	25	3,39
188393	POU domain, class 2, transcription Factor 2	POU2F2	19	24	4,02

Clone ID	Gene/Protein identity	Gene symbol	Chrom. location	N	T/NB
187822	Integrin, beta 2	ITGB2	21q22.3	24	3,01
243907	Nuclear Factor of Activating T cell Subunit p45	NF45	1	24	2,84
158347	EST H27202	EST		23	2,91
230933	EST AW184517	EST		22	2,85
212366	ATP-Binding Cassette, sub-family C (CFTR/MRP), 5	ABCC5	3q27	22	2,70
149401	Cathepsin D	CTSD	11p15.5	21	2,97
	Underexpressed genes				
153854	Desmin	DES	2q35	34	0,00
208717	P55-C-FOS proto-oncogene protein	FOS	14q24.3	33	0,05
159093	Transcription Factor AP4	TFAP4	16p13	33	0,11
124340	Tenascin XA	TNXA	6p21.3	33	0,14
133738	Prolactin	PRL	6p22.2-p21.3	32	0,00
133891	Chorionic Somatomammotropin Hormone 1	CSH1	17q22-q24	32	0,00
151501	Tyrosine Kinase Receptor TEK	TEK	9p21	32	0,00
183030	Activating Transcription Factor 3	ATF3	1	32	0,07
120916	Phosphodiesterase I	PDNP2	8q24.1	32	0,14
155716	EST R72075	EST		31	0,00
208118	Transforming Growth Factor Beta Receptor Type III	TGFB3	1p33-p32	31	0,14
187547	Diphtheria Toxin Receptor	DTR	5q23	31	0,17
108490	HIV-1 Rev Binding protein	HRB	2q36	31	0,20
147002	B-cell CLL/lymphoma 2	BCL2	18q21.3	31	0,26
182610	Microsomal Glutathione S Transferase 1	MGST1	12p12.3-p12.1	31	0,28
152802	Phospholipase A2 Membrane	PLA2G2A	1p35	30	0,03



Clone ID	Gene/Protein identity	Gene symbol	Chrom. location	N	T/NB
	Associated, group IIA				
183087	Interleukin 3 Receptor Alpha chain	IL3RA	Xp22.3;Yp13.3	30	0,24
108571	Retinoblastoma-Like 2 (p130)	RBL2	16q12.2	29	0,28
125294	Adenomatous Polyposis Coli Protein	APC	5q21-q22	29	0,29
151767	FASL Receptor	TNFRSF6	10q24.1	28	0,27

List of the genes that show the most frequent differential expression between normal breast tissue and 34 breast carcinomas as measured by cDNA array analysis. N indicates the number of tumor samples where the gene is dysregulated (fold change > 2) compared to normal breast tissue. T/NB represents the ratio: median expression level in 34 breast tumors / expression level in normal breast. (a) MYBL2 transcript displayed a median expression level of 0.025% in breast tumors and was undetectable in NB.

High expression of mucin 1, NM23, ERBB2, FGFR1 and FGFR2, MYC, stromelysin3, cathepsin D and downregulation of FOS, APC, RBL2, FAS, BCL2 were found, reflecting what is known about their biology in cancer. GATA3, which codes for a member of the GATA family of zinc finger transcription factors, and CRABP2, encoding one of the two cellular retinoic acid-binding proteins, showed high expression of mRNA, extending previous results on cDNA arrays (4).

Differential gene expression among various breast tumors and correlation with histoclinical prognostic parameters

To search for potential prognostic markers in breast cancer, genes with expression levels correlated with conventional histoclinical prognostic parameters were looked for: age of patients, axillary node status, tumor size, histological grade and ER status. No significant correlation was found with age, tumor size and histological grade. However, the expression profiles of some genes correlated with ER status and axillary node involvement.

To identify genes potentially relevant to the hormone-responsive phenotype, the gene expression profiles in ER-positive breast cancers (n = 23) vs ER-negative breast cancers (n = 11) were compared. Sixteen clones displayed a median intensity of 0 in both groups. Twenty-five presented a fold change superior to 2. Table 3a displays the top 10 over- and underexpressed genes. Among them, the most differentially expressed was GATA3 with a median intensity ratio ER+/ER- of 28.6 and a value for the first quartile of ER-positive tumors superior (5-fold) to the value of the third quartile of the ER-negative tumors as shown in Fig. 4a. The high expression of GATA3 in ER-positive tumors was statistically significant using a Mann-Witney test (p 0.001). All ER-positive tumors and only 18% of ER-negative tumors displayed a GATA3 expression level greatly superior (fold change > 3) to the normal breast value. Furthermore GATA3 expression was analyzed by Northern blot hybridization (Fig. 4b) in a panel of 79 breast cancers (21 ER-negative tumors and 58 ER-positive tumors), including 22 of the tumors analyzed with cDNA arrays. It confirmed the array results for those 22 tumors as well as the strong correlation between ER status and GATA3 RNA expression (Mann-Witney test, p ≤ 0.0001).

TABLE 3A

Clone ID	Gene/Protein identity	Gene symbol	ER+/ER-
129757	GATA-binding protein 3	GATA3	28,6
356763	Granzyme A	GZMA	5,7
248613	MYB proto-oncogene	MYB	3,4
211999	KIAA1075 protein	KIAA1075	3,3
235947	Stromelysin 3	STMY3	3,1
229839	Macrophage Stimulating 1	MST1	2,8
153275	Cellular Retinoic Acid Binding Protein 2	CRABP2	2,7
301950	X-box Binding Protein 1	XBP1	2,7
205314	Tumor Protein p53	TP53	2,5
126233	Insulin-like Growth Factor 2	IGF2	2,4
66322	CD3G antigen, Gamma	CD3G	0,0
195022	Interleukin 2 Receptor Gamma chain	IL2RG	0,0
111461	SOX4 Protein	SOX4	0,4
151475	Epidermal Growth Factor Receptor	EGFR	0,5
195022	Interleukin 2 Receptor Beta chain	IL2RB	0,5
130788	Topoisomerase (DNA) II beta (180kD)	TOP2B	0,6
323948	SOX9 Protein	SOX9	0,6
183641	S100 calcium-binding protein Beta	S100B	0,6
246620	EST N53133	EST	0,6
231424	Glutathione S Transferase Pi	GSTP1	0,6

To search for genes whose expression profile was correlated with axillary lymph node status, a strong prognostic factor in breast cancer, the group of node-negative tumors (n = 19) was compared with the group of tumors with massive axillary extension (10 or more positive nodes). Furthermore, because survival decreases with the increase of the number of tumor-involved lymph nodes and because the expression measurements were quantitative, it was looked for a correlation between the expression levels of

these genes and the number of tumor-involved nodes (quantitative variables). Table 3b shows a list of the top 10 over- and underexpressed genes between these 2 groups. Most of these genes have not been previously reported as associated with node status, but some of these results are in agreement with literature data. The gene encoding the tyrosine kinase receptor ERBB2 was the most significantly overexpressed gene in node-positive tumors and displayed the highest correlation coefficient ( $r = 0.68$  ;  $p \leq 0.0001$ ).

TABLE 3B

Clone ID	Gene/Protein identity	Gene symbol	N-/10N+
129757	GATA-binding protein 3	GATA3	11,0
160963	Thrombospondin 1	THBS1	6,6
151475	Epidermal Growth Factor Receptor	EGFR	5,4
120916	Phosphodiesterase I	PDNP2	4,9
183030	Activating Transcription Factor 3	ATF3	4,6
211999	KIAA1075 protein	KIAA1075	4,5
110480	Nuclear Factor 1 A-type	NF1A	4,5
182264	P-Selectin	SELP	4,4
356763	Granzyme A	GZMA	4,3
214008	E-cadherin	CDH1	4,0
147016	ERBB2 Receptor Protein-Tyrosine Kinase	ERBB2	0,2
179197	Protein Phosphatase PP2A, 55 kD Subunit	PP2A BR gamma	0,2
231424	Glutathione S Transferase Pi	GSTP1	0,4
111461	SOX4 Protein	SOX4	0,4
195022	Interleukin 2 Receptor Beta chain	IL2RB	0,4
220451	Zinc Finger protein 144	ZNF144	0,5
125413	Mucin 1	MUC1	0,6
290007	CD44 antigen, epithelial form	CD44	0,6
108571	Retinoblastoma-Like 2 (p130)	RBL2	0,7
130788	Topoisomerase (DNA) II Beta (180kD)	TOP2B	0,7

### Gene clusters

Gene clustering from Fig. 2b showed groups of genes with correlated expression across samples. When different clones represented the same gene, they were

clustered next to each other (red arrows). Correlation coefficients between gene pairs in the 34 tumors were often high (1% of the 13,041 gene pairs showed a correlation coefficient superior to 0.95 - not shown). An example of highly correlated gene expression is that of BCL2 and RBL2. Such correlated expression, although it has not been described in the literature, probably reflects a common mechanism of regulation for these two genes. Furthermore, these genes also exhibited significant correlated expression with other genes such as PPP2CA, AKT2, PRKCSH or TNFRSF6/FAS. In particular, a striking correlated expression between BCL2 and FAS could be observed ( $r = 0.91$ ; data not shown). The exact meaning of this correlation is unknown, although it may reflect the necessary balance between apoptosis and anti-apoptosis for cell survival.

Although in human cancer the proportion of changes that is reflected at the RNA level is not known, monitoring gene expression patterns appears as a very promising way of increasing the knowledge of the disease. Several different types of cancer have been investigated using cDNA arrays: cervical (14), hepatocellular (15), ovarian (16), colon (17) and renal carcinomas (18), glioblastomas (19), melanomas (20) (21), rhabdomyosarcomas (22), acute leukemias (23) and lymphomas (24). In breast cancer, pioneering studies have yielded the first expression patterns (4, 25-31). They have in particular addressed the important issue of molecular differences in hormone responsive and non-responsive breast tumors. Thus, Yang et al. (28) and Hoch et al. (25) compared expression profiles of breast carcinoma cell lines known to represent these two categories and identified a few genes with differential expression. One of these genes was GATA3. In these studies, cell lines were mostly used and tumor samples were rarely

tested and generally in small numbers. The first study analyzing the expression profiles of a large series of breast cancers was published recently (32), but no correlation with clinical outcome was mentioned.

5               Several interesting points can be made based on the present experimentation. First, the differences in expression patterns among the tumors provided molecular transcriptional evidence of the histoclinical heterogeneity of breast cancer. This diversity was multifactorial, linked  
10 to many different genes, highlighting the interest of high throughput analysis in this context. It was possible, with a hierarchical clustering program integrating the expression profiles, to separate normal breast tissue from most tumors and, moreover, to identify two different groups of tumors.  
15 Most importantly, two different subgroups of tumors with a very distinct clinical outcome that could not be predicted with classical prognostic factors have been identified by clustering. Indeed, all these tumors had a theoretically bad prognosis as evaluated by current histoclinical tools. All  
20 these patients would be at the present time treated with adjuvant chemotherapy, but without the capacity for the physicians to identify patients who will benefit of this treatment and those who will not benefit.

Gene expression profiles were able to make this  
25 discrimination. Such predictive tools have important therapeutic implications. Patients with features of poor prognosis are candidates for other treatment than standard chemotherapy, avoiding loss of time and toxicities related to first-line chemotherapy. These results suggest that the  
30 histoclinical category of poor prognosis breast cancer, currently treated with adjuvant anthracyclin-based chemotherapy, groups together at least two molecularly distinct subgroups of tumors with different outcome which

would require distinct chemotherapy regimens. Expression profiles could thus provide a new and more accurate way of classifying breast tumors of poor prognosis and managing patients.

5                   Similarly, despite molecular heterogeneity, significant correlations between the expression level of genes (GATA3, ERBB2) and histological tumor parameters were identified. The ER-positivity in breast cancer has been correlated with tumor differentiation, low proliferating rate, favorable prognosis and response to hormonal therapy. 10 The relation between hormone sensitivity of breast cancer and ER status is not perfect, and it is possible that some genes related to ER expression are more important than ER to characterize the hormone sensitive phenotype. These genes 15 could serve as predictive factors to guide the therapy.

GATA3 mRNA expression was highly correlated with ER status. GATA3, which is not estrogen-regulated (25), is a transcription factor that could regulate the expression of genes involved in the ER-positive phenotype. Among the other 20 genes that were found associated with ER status during the experimental work leading to the present invention, some, such as MYB (10), stromelysin 3 (33), and CRABP2 (34), have been previously reported expressed at high levels in ER-positive breast tumors. The higher levels of TP53 mRNA in 25 ER-positive tumors studied were surprising, although in agreement with a recent study (27). Most studies concerning TP53 expression analyzed the protein level rather than the mRNA level, and TP53 protein levels are classically negatively correlated with the ER status (35). The high 30 expression of CRABP2 could be related to the better differentiated status of the ER-positive tumors. The low expression of the three immunity-related genes IL2RB, IL2RG and CD3G may be related to the low lymphoid infiltration in

these well differentiated tumors. ERBB2 high expression in breast cancer has been associated with a poor prognosis and some resistance to hormonal therapy and chemotherapy (36). It is involved in the regulation of cellular differentiation, adhesion, and motility. The motility-enhancing activity of ERBB2 (37) could be responsible for the increased metastatic potential and the unfavorable prognosis of the breast tumors that overexpress ERBB2. The low expression of E-cadherin and thrombospondin 1 in node-positive tumors are consistent with their putative role in different steps of metastatic spread: E-cadherin is an epithelial cell adhesion molecule whose disturbance is a prerequisite for the release of invasive cells in carcinomas (38) and thrombospondin 1 inhibits angiogenesis (39). Similarly, the high expression of the molecule surface antigen Mucin 1 in node-positive tumors (40) can reduce cell-cell interactions facilitating cell detachment and metastasis. CD44, encoding a transmembrane glycoprotein involved in cell adhesion and lymph node homing (41) was expressed at high levels in node-positive tumors as well as GSTP1 (Glutathione-S-Transferase Pi), recently reported associated with increased tumor size (27).

Second, there were a number of genes with highly correlated expression patterns. Gene correlations have already been reported with larger series of genes, essentially under dynamic experimental conditions (42) and recently in steady states (17). Here, correlations were based on expression profiles of a relatively small but selected series of genes and in steady states represented by different breast tumors. Gene correlations are potentially useful tools for cancer research in two ways: i)- they can provide information about the general regulation circuitry of a cancerous cell, allowing the identification of regulatory elements controlling expression networks; ii)- they offer the



possibility of reducing the complexity of the system analyzed by replacing, for example, the intensities of a large number of genes present in a gene cluster by their respective mean intensities.

5                   Finally, these results highlight the great potential of cDNA array in cancer research. The gene expression profiles confirmed the heterogeneity of breast cancer, and most importantly allowed us to identify, among a series of poor prognosis breast tumors, two subtypes of the  
10                   disease not yet recognized with usual histoclinical parameters but with a different clinical outcome after adjuvant chemotherapy. Furthermore, the present invention allows detecting genes of which expression was correlated with classical prognostic factors.

15                   Table 4 displays a library of polynucleotides SEQ ID NO :1 to SEQ ID NO : 468 corresponding to a population of polynucleotide sequences underexpressed or overexpressed in cells derived from tumors, more particularly breast tumors,  
20                   and their respective complements.

TABLE 4

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
HRB	1	hiv-1 rev binding protein	SEQ ID No:1		SEQ ID No:2
GATA1	2	gata-binding protein 1 (globin transcription factor 1)		SEQ ID No:3	SEQ ID No:4
TLK2	3	tousled-like kinase 2		SEQ ID No:5	SEQ ID No:6
EST T81919	4	ests, weakly similar to alu7_human alu subfamily sq sequence contamination warning entry [h.sapiens]	SEQ ID No:7	SEQ ID No:8	
CCND1	5	cyclin d1 (prad1: parathyroid adenomatosis 1)	SEQ ID No:9		SEQ ID No:10
STAT1	6	signal transducer and activator of transcription 1, 91kd		SEQ ID No:11	SEQ ID No:12
FGFR2	7	fibroblast growth factor receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome)	SEQ ID No:13	SEQ ID No:14	SEQ ID No:15
EST T89980	8	ests	SEQ ID No:16		
PPP3CC	9	protein phosphatase 3 (formerly 2b), catalytic subunit, gamma isoform (calcineurin a gamma)	SEQ ID No:17	SEQ ID No:18	SEQ ID No:19
EST T90726	10	ests	SEQ ID No:20	SEQ ID No:21	
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
RNF5	12	ring finger protein 5		SEQ ID No:25	SEQ ID No:26
AXL	13	axl receptor tyrosine kinase	SEQ ID No:27	SEQ ID No:28	SEQ ID No:29
CTSB	14	cathepsin b		SEQ ID No:30	SEQ ID No:31
PPP4C	15	protein phosphatase 4 (formerly x), catalytic subunit	SEQ ID No:32	SEQ ID No:33	SEQ ID No:34
EST T79867	16	ests	SEQ ID No:35		
FGFR4	17	fibroblast growth factor receptor 4	SEQ ID No:36	SEQ ID No:37	SEQ ID No:38
ENPP2	18	ectonucleotide pyrophosphatase/phosphodiesterase 2	SEQ ID No:39	SEQ ID No:40	SEQ ID No:41

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		(autotaxin)			
RELA	19	v-rel avian reticuloendotheliosis viral oncogene homolog a (nuclear factor of kappa light polypeptide gene enhancer in b-cells 3 (p65))	SEQ ID No:42		SEQ ID No:43
ITK	20	il2-inducible t-cell kinase		SEQ ID No:44	SEQ ID No:45
TNXB	21	tenascin xb		SEQ ID No:46	SEQ ID No:47
CSF1	22	colony stimulating factor 1 (macrophage)	SEQ ID No:48	SEQ ID No:49	SEQ ID No:50
VIL2	23	villin 2 (ezrin)	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
APC	24	adenomatosis polyposis coli	SEQ ID No:54	SEQ ID No:55	SEQ ID No:56
MUC1	25	mucin 1, transmembrane		SEQ ID No:57	SEQ ID No:58
IGF2	26	insulin-like growth factor 2 (somatomedin a)	SEQ ID No:59	SEQ ID No:60	SEQ ID No:61
EMR1	27	egf-like module containing, mucin-like, hormone receptor-like sequence 1	SEQ ID No:62	SEQ ID No:63	SEQ ID No:64
KIAA0427	28	kiaa0427 gene product	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
SYK	29	spleen tyrosine kinase	SEQ ID No:68	SEQ ID No:69	SEQ ID No:70
IL7R	30	interleukin 7 receptor		SEQ ID No:71	SEQ ID No:72
MYC	31	v-myc avian myelocytomatosis viral oncogene homolog	SEQ ID No:73	SEQ ID No:74	SEQ ID No:75
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
GRB7	33	growth factor receptor-bound protein 7	SEQ ID No:79	SEQ ID No:80	SEQ ID No:81
TOP2B	34	topoisomerase (dna) ii beta (180kd)		SEQ ID No:82	SEQ ID No:83
CASP4	35	caspase 4, apoptosis-related cysteine protease	SEQ ID No:84		SEQ ID No:85
TIMP2	36	tissue inhibitor of metalloproteinase 2		SEQ ID No:86	SEQ ID No:87
DDT	37	d-dopachrome tautomerase	SEQ ID No:88	SEQ ID No:89	SEQ ID No:90
PRL	38	prolactin	SEQ ID	SEQ ID	SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
			No:91	No:92	No:93
PRLR	39	prolactin receptor	SEQ ID No:94	SEQ ID No:95	SEQ ID No:96
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
GATA3	41	gata-binding protein 3	SEQ ID No:100	SEQ ID No:101	SEQ ID No:78
PGF	42	placental growth factor, vascular endothelial growth factor-related protein		SEQ ID No:102	SEQ ID No:103
UBE3A	43	ubiquitin protein ligase e3a (human papilloma virus e6-associated protein, angelman syndrome)		SEQ ID No:104	SEQ ID No:105
TC21	44	oncogene tc21	SEQ ID No:106	SEQ ID No:107	SEQ ID No:108
TIE	45	tyrosine kinase with immunoglobulin and epidermal growth factor homology domains		SEQ ID No:109	SEQ ID No:110
AMFR	46	autocrine motility factor receptor	SEQ ID No:111	SEQ ID No:112	SEQ ID No:113
EST R81127	47	homo sapiens mrna; cdna dkfzp434c136 (from clone dkfzp434c136)	SEQ ID No:114		
BCL2	48	b-cell cll/lymphoma 2	SEQ ID No:115	SEQ ID No:116	SEQ ID No:117
ERBB2	49	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)		SEQ ID No:118	SEQ ID No:119
MDM2	50	mouse double minute 2, human homolog of; p53-binding protein		SEQ ID No:120	SEQ ID No:121
GATA3	51	gata-binding protein 3	SEQ ID No:122		SEQ ID No:78
HIP-55	52	src homology 3 domain-containing protein hip-55	SEQ ID No:123	SEQ ID No:124	SEQ ID No:125
CTSD	53	cathepsin d (lysosomal aspartyl protease)	SEQ ID No:126	SEQ ID No:127	SEQ ID No:128
IGF1R	54	insulin-like growth factor 1 receptor		SEQ ID No:129	SEQ ID No:130
INSR	55	insulin receptor		SEQ ID No:131	SEQ ID No:132
FOXO1A	56	forkhead box o1a (rhabdomyosarcoma)		SEQ ID No:133	SEQ ID No:134
EGFR	57	epidermal growth factor receptor	SEQ ID	SEQ ID	SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		(avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	No:135	No:136	No:137
TEK	58	tek tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal)	SEQ ID No:138	SEQ ID No:139	SEQ ID No:140
TNFRSF6	59	tumor necrosis factor receptor superfamily, member 6	SEQ ID No:141	SEQ ID No:142	SEQ ID No:143
CDKN1A	60	cyclin-dependent kinase inhibitor 1a (p21, cip1)	SEQ ID No:144	SEQ ID No:145	SEQ ID No:146
PLA2G2A	61	phospholipase a2, group iia (platelets, synovial fluid)	SEQ ID No:147	SEQ ID No:148	SEQ ID No:149
GAPD	62	glyceraldehyde-3-phosphate dehydrogenase	SEQ ID No:150	SEQ ID No:151	SEQ ID No:152
JUNB	63	jun b proto-oncogene	SEQ ID No:153	SEQ ID No:154	SEQ ID No:155
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
ACVRL1	65	activin a receptor type ii-like 1	SEQ ID No:159	SEQ ID No:160	SEQ ID No:161
RIL	66	lim domain protein		SEQ ID No:162	SEQ ID No:163
SHC1	67	shc (src homology 2 domain-containing) transforming protein 1		SEQ ID No:164	SEQ ID No:165
GAPD	68	glyceraldehyde-3-phosphate dehydrogenase	SEQ ID No:166	SEQ ID No:167	SEQ ID No:152
DES	69	desmin	SEQ ID No:168	SEQ ID No:169	SEQ ID No:170
CSNK2B	70	casein kinase 2, beta polypeptide		SEQ ID No:171	SEQ ID No:172
GLG1	71	golgi apparatus protein 1	SEQ ID No:173	SEQ ID No:174	SEQ ID No:175
EDNRB	72	endothelin receptor type b		SEQ ID No:176	SEQ ID No:177
GZMB	73	granzyme b (granzyme 2, cytotoxic t-lymphocyte-associated serine esterase 1)	SEQ ID No:178		SEQ ID No:179
FGFR1	74	fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, pfeiffer syndrome)	SEQ ID No:180	SEQ ID No:181	SEQ ID No:182
PPP2CA	75	protein phosphatase 2 (formerly 2a), catalytic subunit, alpha isoform		SEQ ID No:183	SEQ ID No:184
EST R55460	76	homo sapiens, clone image:4054156, mRNA, partial cds		SEQ ID No:185	

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
IGKC	77	immunoglobulin kappa constant	SEQ ID No:186		
MC1R	78	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor)		SEQ ID No:187	SEQ ID No:188
NRG1	79	neuregulin 1	SEQ ID No:189	SEQ ID No:190	SEQ ID No:191
CNTFR	80	ciliary neurotrophic factor receptor		SEQ ID No:192	SEQ ID No:193
ANG	81	angiogenin, ribonuclease, rnase a family, 5		SEQ ID No:194	SEQ ID No:195
ENG	82	endoglin (osler-rendu-weber syndrome 1)	SEQ ID No:196	SEQ ID No:197	SEQ ID No:198
EGF	83	epidermal growth factor (beta-urogastrone)	SEQ ID No:199		SEQ ID No:200
HRMT1L1	84	hmt1 (hnrrnp methyltransferase, s. cerevisiae)-like 1	SEQ ID No:201	SEQ ID No:202	SEQ ID No:203
ETV4	85	ets variant gene 4 (ela enhancer-binding protein, elaf)	SEQ ID No:204	SEQ ID No:205	
ANXA11	86	annexin a11		SEQ ID No:206	SEQ ID No:207
PDGFRB	87	platelet-derived growth factor receptor, beta polypeptide		SEQ ID No:208	SEQ ID No:209
WBSCR14	88	williams-beuren syndrome chromosome region 14		SEQ ID No:210	SEQ ID No:211
CD74	89	cd74 antigen (invariant polypeptide of major histocompatibility complex, class ii antigen-associated)		SEQ ID No:212	SEQ ID No:213
ANXA7	90	annexin a7		SEQ ID No:214	SEQ ID No:215
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
PTPN2	92	protein tyrosine phosphatase, non-receptor type 2	SEQ ID No:218	SEQ ID No:219	SEQ ID No:220
EPHA2	93	epha2	SEQ ID No:221		SEQ ID No:222
TIMP1	94	tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor)	SEQ ID No:223	SEQ ID No:224	SEQ ID No:225
EFNA1	95	ephrin-a1		SEQ ID No:226	SEQ ID No:227

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
EDNRA	96	endothelin receptor type a	SEQ ID No:228		SEQ ID No:229
GRB2	97	growth factor receptor-bound protein 2	SEQ ID No:230	SEQ ID No:231	SEQ ID No:232
JUND	98	jun d proto-oncogene	SEQ ID No:233		SEQ ID No:234
SMARCA2	99	swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	SEQ ID No:235	SEQ ID No:236	SEQ ID No:237
PPP2R2C	100	protein phosphatase 2 (formerly 2a), regulatory subunit b (pr 52), gamma isoform	SEQ ID No:238	SEQ ID No:239	
THBS3	101	thrombospondin 3	SEQ ID No:240		SEQ ID No:241
ACTG1	102	actin, gamma 1	SEQ ID No:242	SEQ ID No:243	SEQ ID No:244
ITGA6	103	integrin, alpha 6	SEQ ID No:245	SEQ ID No:246	SEQ ID No:247
RAD9	104	rad9 (s. pombe) homolog	SEQ ID No:248		SEQ ID No:249
ATF3	105	activating transcription factor 3	SEQ ID No:250	SEQ ID No:251	SEQ ID No:252
AKT2	106	v-akt murine thymoma viral oncogene homolog 2	SEQ ID No:253		SEQ ID No:254
S100B	107	s100 calcium-binding protein, beta (neural)		SEQ ID No:255	SEQ ID No:256
ABCB1	108	atp-binding cassette, sub-family b (mdr/tap), member 1	SEQ ID No:257		SEQ ID No:258
SELE	109	selectin e (endothelial adhesion molecule 1)	SEQ ID No:259	SEQ ID No:260	SEQ ID No:261
EGF	110	epidermal growth factor (beta-urogastrone)	SEQ ID No:262		SEQ ID No:200
PRKCSH	111	protein kinase c substrate 80k-h		SEQ ID No:263	SEQ ID No:264
DTR	112	diphtheria toxin receptor (heparin-binding epidermal growth factor-like growth factor)		SEQ ID No:265	SEQ ID No:266
ITGB2	113	integrin, beta 2 (antigen cd18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit)		SEQ ID No:267	SEQ ID No:268
NEO1	114	neogenin (chicken) homolog 1		SEQ ID No:269	SEQ ID No:270
POU2F2	115	pou domain, class 2, transcription	SEQ ID		SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		factor 2	No:271		No:272
BIRC4	116	baculoviral iap repeat-containing 4	SEQ ID No:273		SEQ ID No:274
DAP3	117	death associated protein 3	SEQ ID No:275		SEQ ID No:276
GNRH1	118	gonadotropin-releasing hormone 1 (leutinizing-releasing hormone)		SEQ ID No:277	SEQ ID No:278
IL2RG	119	interleukin 2 receptor, gamma (severe combined immunodeficiency)	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
DAP3	120	death associated protein 3	SEQ ID No:282	SEQ ID No:283	SEQ ID No:276
PTK2	121	ptk2 protein tyrosine kinase 2		SEQ ID No:284	SEQ ID No:285
CDK4	122	cyclin-dependent kinase 4	SEQ ID No:286	SEQ ID No:287	SEQ ID No:288
BTF3	123	basic transcription factor 3	SEQ ID No:289		SEQ ID No:290
CSF1R	124	colony stimulating factor 1 receptor, formerly mcdonough feline sarcoma viral (v-fms) oncogene homolog	SEQ ID No:291		SEQ ID No:292
FLI1	125	friend leukemia virus integration 1	SEQ ID No:293	SEQ ID No:294	SEQ ID No:295
EST R97218	126	ests, highly similar to tvhume hepatocyte growth factor receptor precursor [h.sapiens]	SEQ ID No:296	SEQ ID No:297	
ETV5	127	ets variant gene 5 (ets-related molecule)	SEQ ID No:298	SEQ ID No:299	SEQ ID No:300
CDK4	128	cyclin-dependent kinase 4	SEQ ID No:301	SEQ ID No:302	SEQ ID No:288
YES1	129	v-yes-1 yamaguchi sarcoma viral oncogene homolog 1	SEQ ID No:303		SEQ ID No:304
IFI75	130	interferon-induced protein 75, 52kd	SEQ ID No:305	SEQ ID No:306	SEQ ID No:307
MYBL2	131	v-myb avian myeloblastosis viral oncogene homolog-like 2	SEQ ID No:308	SEQ ID No:309	SEQ ID No:310
TGFBR3	132	transforming growth factor, beta receptor iii (betaglycan, 300kd)	SEQ ID No:311	SEQ ID No:312	SEQ ID No:313
PRDX2	133	peroxiredoxin 2	SEQ ID No:314	SEQ ID No:315	SEQ ID No:316
FOS	134	v-fos fbj murine osteosarcoma viral oncogene homolog		SEQ ID No:317	SEQ ID No:318



Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
RBBP7	135	retinoblastoma-binding protein 7	SEQ ID No:319	SEQ ID No:320	SEQ ID No:321
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
ABCC5	137	atp-binding cassette, sub-family c (cftr/mrp), member 5		SEQ ID No:324	SEQ ID No:325
CDH1	138	cadherin 1, type 1, e-cadherin (epithelial)	SEQ ID No:326	SEQ ID No:327	SEQ ID No:328
ZNF144	139	zinc finger protein 144 (mel-18)		SEQ ID No:329	SEQ ID No:330
MST1	140	macrophage stimulating 1 (hepatocyte growth factor-like)	SEQ ID No:331	SEQ ID No:332	SEQ ID No:333
GSTP1	141	glutathione s-transferase pi	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336
BCL2	142	b-cell cll/lymphoma 2	SEQ ID No:337	SEQ ID No:338	SEQ ID No:117
PCNA	143	proliferating cell nuclear antigen	SEQ ID No:339	SEQ ID No:340	SEQ ID No:341
BS69	144	adenovirus 5 ela binding protein	SEQ ID No:342	SEQ ID No:343	SEQ ID No:344
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
MGC13071	146	hypothetical protein mgc13071	SEQ ID No:347	SEQ ID No:348	SEQ ID No:349
ILF2	147	interleukin enhancer binding factor 2, 45kd		SEQ ID No:350	SEQ ID No:351
FLJ11307	148	hypothetical protein flj11307	SEQ ID No:352		SEQ ID No:353
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
ZNF9	150	zinc finger protein 9 (a cellular retroviral nucleic acid binding protein)	SEQ ID No:356		SEQ ID No:357
CREM	151	camp responsive element modulator	SEQ ID No:358	SEQ ID No:359	SEQ ID No:360
CTSB	152	cathepsin b	SEQ ID No:361		SEQ ID No:31
MLANA	153	melan-a	SEQ ID No:362	SEQ ID No:363	SEQ ID No:364
APR-1	154	apr-1 protein	SEQ ID No:365	SEQ ID No:366	SEQ ID No:367
ETV5	155	ets variant gene 5 (ets-related	SEQ ID	SEQ ID	SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		molecule)	No:368	No:369	No:300
CD69	156	cd69 antigen (p60, early t-cell activation antigen)		SEQ ID No:370	SEQ ID No:371
TC21	157	oncogene tc21	SEQ ID No:372	SEQ ID No:373	SEQ ID No:108
CD44	158	cd44 antigen (homing function and indian blood group system)	SEQ ID No:374	SEQ ID No:375	SEQ ID No:376
CDKN3	159	cyclin-dependent kinase inhibitor 3 (cdk2-associated dual specificity phosphatase)	SEQ ID No:377	SEQ ID No:378	SEQ ID No:379
MXI1	160	max-interacting protein 1		SEQ ID No:380	SEQ ID No:381
HOXA5	161	homeo box a5	SEQ ID No:382	SEQ ID No:383	SEQ ID No:384
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
TNFAIP3	163	tumor necrosis factor, alpha-induced protein 3	SEQ ID No:388	SEQ ID No:389	SEQ ID No:390
SRF	164	serum response factor (c-fos serum response element-binding transcription factor)	SEQ ID No:391	SEQ ID No:392	SEQ ID No:393
SOX9	165	sry (sex determining region y)-box 9 (campomelic dysplasia, autosomal sex-reversal)	SEQ ID No:394		SEQ ID No:395
CDH15	166	cadherin 15, m-cadherin (myotubule)	SEQ ID No:396	SEQ ID No:397	SEQ ID No:398
BCL2	167	b-cell cll/lymphoma 2	SEQ ID No:399	SEQ ID No:400	SEQ ID No:117
EST W73386	168	ests	SEQ ID No:401		
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403
FOS	170	v-fos fbj murine osteosarcoma viral oncogene homolog	SEQ ID No:404	SEQ ID No:405	SEQ ID No:318
ILF1	171	interleukin enhancer binding factor 1	SEQ ID No:406	SEQ ID No:407	SEQ ID No:408
ARHGDIA	172	rho gdp dissociation inhibitor (gdi) alpha	SEQ ID No:409	SEQ ID No:410	SEQ ID No:411
C4A	173	complement component 4a	SEQ ID No:412		SEQ ID No:413
CD3G	174	cd3g antigen, gamma polypeptide (tit3 complex)	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
RELB	175	v-rel avian reticuloendotheliosis viral oncogene homolog b (nuclear factor of kappa light polypeptide gene enhancer in b-cells 3)	SEQ ID No:417	SEQ ID No:418	SEQ ID No:419
ESR1	176	estrogen receptor 1	SEQ ID No:420	SEQ ID No:421	SEQ ID No:422
PBX1	177	pre-b-cell leukemia transcription factor 1	SEQ ID No:423	SEQ ID No:424	SEQ ID No:425
GLI3	178	gli-kruppel family member gli3 (greig cephalopolysyndactyly syndrome)	SEQ ID No:426	SEQ ID No:427	SEQ ID No:428
ILF1	179	interleukin enhancer binding factor 1	SEQ ID No:429		SEQ ID No:408
EST T80406	180	similar to SP:S36648 S36648 RB2/P130 PROTEIN	SEQ ID No:430		
EST T95640	181	similar to gb:M16336 T-CELL SURFACE ANTIGEN CD2	SEQ ID No:431		
EST R28523	182	similar to placental lactogen (CSH1)	SEQ ID No:432		
ESTs H21879 & H21880	183	Homo sapiens plasminogen activator (PLAT)	SEQ ID No:433	SEQ ID No:434	
ESTs H24628 & H24592	184	Homo sapiens aminoacylase 1 (ACY1)	SEQ ID No:435	SEQ ID No:436	
EST H28056	185	Homo sapiens E74-like factor 1 (ets domain transcription factor) (ELF1)	SEQ ID No:437		
ESTs H30141 & H27466	186	Homo sapiens selectin P	SEQ ID No:438	SEQ ID No:439	
ESTs H42957 & H42888	187	Human interleukin 3 receptor (hIL-3Ra)	SEQ ID No:440	SEQ ID No:441	
EST H57912	188	Human tumor protein p53 (Li-Fraumeni syndrome) (TP53)	SEQ ID No:442	SEQ ID No:443	
ERBB2	189	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog) (ERBB2)	SEQ ID No:444		
ZNF144	190	zinc finger protein 144 (Mel-18) (ZNF144)	SEQ ID No:445		

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
MARK3	191	MAP/microtubule affinity-regulating kinase 3 (MARK3)	SEQ ID No:446	SEQ ID No:447	
EST N68536	192	EST N68536 MAX-interacting protein 1 (MXI1)	SEQ ID No:448		
EST R81126	193	EST R81126 lymphotoxin beta receptor (LTBR)		SEQ ID No:449	
POU2F2	194	(POU2F2)		SEQ ID No:450	
CASP1	195	caspase 4, apoptosis-related cysteine protease (CASP4) (ex CASP1)		SEQ ID No:451	
HRB	196	syndecan 1 (SDC1) (ex HRB)		SEQ ID No:452	
ITGB2	197	integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit) (ITGB2)	SEQ ID No:453		
MGST1	198	protein phosphatase 1, catalytic subunit, alpha isoform (PPP1CA) (ex MGST1)		SEQ ID No:454	
PPP2CA	199	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform (PPP2CA)	SEQ ID No:455		
SUI1	200	S100 calcium-binding protein A11 (calgizzarin) (S100A11)		SEQ ID No:456	
GZMA	201	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3) (GZMA)		SEQ ID No:457	
EDN1	202	endothelin 1 (EDN1)	SEQ ID No:458		
PTPN6	203	protein tyrosine phosphatase, non-receptor type 6 (PTPN6)	SEQ ID No:459		
TFAP4	204	transcription factor AP-4 (activating enhancer binding protein 4) (TFAP4)	SEQ ID No:460		
CCND2	205	cyclin D2 (CCND2)	SEQ ID No:461		
JUP	206	junction plakoglobin (JUP)	SEQ ID No:462		
GADD45A	207	growth arrest and DNA-damage-inducible, alpha (GADD45A)	SEQ ID No:463		
nm23	208	non-metastatic cells 1, protein (NM23A) expressed in (NME1)	SEQ ID No:464		
BBC1	209	ribosomal protein L13 (RPL13) (ex	SEQ ID		

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		BBC1)	No:465		
VEGFB	210	vascular endothelial growth factor B (VEGFB)	SEQ ID No:466		
LAMR1	211	laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1)	SEQ ID No:467		
CSH1	212	Chorionic somatomammotropin hormone 1 (placental lactogen) = LACTOGEN Precursor		SEQ ID No:468	

Tables 5A and 5B hereunder displays two subpopulations corresponding to the 5 top overexpressed and to the 5 top underexpressed polynucleotide sequences particularly interesting to distinguish healthy person from cancer patient.

TABLE 5A

overexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
GZMB	73	granzyme b (granzyme 2, cytotoxic t-lymphocyte-associated serine esterase 1)	SEQ ID No:178		SEQ ID No:179
MYBL2	131	v-myb avian myeloblastosis viral oncogene homolog-like 2	SEQ ID No:308	SEQ ID No:309	SEQ ID No:310
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
EST T95640	181	similar to gb:M16336 T-CELL SURFACE ANTIGEN CD2	SEQ ID No:431		

**TABLE 5B**  
underexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
PRL	38	prolactin	SEQ ID No:91	SEQ ID No:92	SEQ ID No:93
TEK	58	tek tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal)	SEQ ID No:138	SEQ ID No:139	SEQ ID No:140
PLA2G2A	61	phospholipase a2, group iia (platelets, synovial fluid)	SEQ ID No:147	SEQ ID No:148	SEQ ID No:149
DES	69	desmin	SEQ ID No:168	SEQ ID No:169	SEQ ID No:170
EST R28523	182	similar to placental lactogen (CSH1)	SEQ ID No:432		

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Table 6 hereunder relate to sub populations of polynucleotide sequences interesting to detect hormone sensitive tumors allowing to distinguish between ER+ and ER- samples.

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**TABLE 6**

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
IGF2	26	insulin-like growth factor 2 (somatomedin a)	SEQ ID No:59	SEQ ID No:60	SEQ ID No:61
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
TOP2B	34	topoisomerase (dna) ii beta (180kd)		SEQ ID No:82	SEQ ID No:83
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
S100B	107	s100 calcium-binding protein, beta (neural)		SEQ ID No:255	SEQ ID No:256
IL2RG	119	interleukin 2 receptor, gamma (severe combined immunodeficiency)	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
MST1	140	macrophage stimulating 1 (hepatocyte growth factor-like)	SEQ ID No:331	SEQ ID No:332	SEQ ID No:333
GSTP1	141	glutathione s-transferase pi	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
FLJ11307	148	hypothetical protein flj11307	SEQ ID No:352		SEQ ID No:353
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
SOX9	165	sry (sex determining region y)-box 9 (campomelic dysplasia, autosomal sex-reversal)	SEQ ID No:394		SEQ ID No:395
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403
CD3G	174	cd3g antigen, gamma polypeptide (tit3 complex)	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416
EST H57912	188	Human tumor protein p53 (Li-Fraumeni syndrome) (TP53)	SEQ ID No:442		

Tables 6A et 6B hereunder relate to two sub populations of polynucleotide sequences particularly interesting to detect hormone sensitive tumors allowing to distinguish between ER+ and ER- samples

Table 6A

overexpressed genes : top 5

ER + / ER -

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403

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Table 6B

underexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y) - box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
IL2RG	119	interleukin 2 receptor, gamma (severe combined immunodeficiency)	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
CD3G	174	cd3g antigen, gamma polypeptide (tit3 complex)	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416

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Tables 7 hereunder relates to subpopulations of polynucleotide sequences interesting to distinguish tumors with lymph node from tumors with no lymph node.



TABLE 7

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
EST T89980	8	ests	SEQ ID No:16		
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
ENPP2	18	ectonucleotide pyrophosphatase/phosphodiesterase (autotaxin)	SEQ ID No:39	SEQ ID No:40	SEQ ID No:41
MUC1	25	mucin 1, transmembrane		SEQ ID No:57	SEQ ID No:58
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
TOP2B	34	topoisomerase (dna) ii beta (180kd)		SEQ ID No:82	SEQ ID No:83
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
ERBB2	49	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)		SEQ ID No:118	SEQ ID No:119
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
PPP2R2C	100	protein phosphatase 2 (formerly 2a), regulatory subunit b (pr 52), gamma isoform	SEQ ID No:238	SEQ ID No:239	
ATF3	105	activating transcription factor 3	SEQ ID No:250	SEQ ID No:251	SEQ ID No:252
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
CDH1	138	cadherin 1, type 1, e-cadherin (epithelial)	SEQ ID No:326	SEQ ID No:327	SEQ ID No:328
ZNF144	139	zinc finger protein 144 (mel-18)		SEQ ID No:329	SEQ ID No:330
GSTP1	141	glutathione s-transferase pi	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336
CD44	158	cd44 antigen (homing function and indian blood group system)	SEQ ID No:374	SEQ ID No:375	SEQ ID No:376
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
EST T80406	180	similar to SP:S36648 S36648 RB2/P130 PROTEIN	SEQ ID No:430		
ESTs H30141 & H27466	186	Homo sapiens selectin P	SEQ ID No:438	SEQ ID No:439	

Tables 7A and 7B hereunder relate to two sub populations of polynucleotide sequences particularly interesting to distinguish tumors with lymph node from tumors with no lymph node.

**TABLE 7A**

Overexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
ENPP2	18	ectonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin)	SEQ ID No:39	SEQ ID No:40	SEQ ID No:41
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
ATF3	105	activating transcription factor 3	SEQ ID No:250	SEQ ID No:251	SEQ ID No:252

**TABLE 7B**

Underexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
ERBB2	49	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)		SEQ ID No:118	SEQ ID No:119
PPP2R2C	100	protein phosphatase 2 (formerly 2a), regulatory subunit b (pr 52), gamma isoform	SEQ ID No:238	SEQ ID No:239	
GSTP1	141	glutathione s-transferase pi	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336

Tables 8, 8A and 8B hereunder relates to sub populations of polynucleotide sequences particularly interesting to distinguish tumors sensitive to antracycline from tumors unsensitive to antracycline.

TABLE 8

A1 /A2

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
CSF1	22	colony stimulating factor 1 (macrophage)	SEQ ID No:48	SEQ ID No:49	SEQ ID No:50
VIL2	23	villin 2 (ezrin)	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
IGF2	26	insulin-like growth factor 2 (somatomedin a)	SEQ ID No:59	SEQ ID No:60	SEQ ID No:61
KIAA0427	28	kiaa0427 gene product	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
MYC	31	v-myc avian myelocytomatosis viral oncogene homolog	SEQ ID No:73	SEQ ID No:74	SEQ ID No:75
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
TOP2B	34	topoisomerase (dna) ii beta (180kd)		SEQ ID No:82	SEQ ID No:83
ERBB2	49	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog)		SEQ ID No:118	SEQ ID No:119
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
GZMB	73	granzyme b (granzyme 2, cytotoxic t-lymphocyte-associated serine esterase 1)	SEQ ID No:178		SEQ ID No:179
IGKC	77	immunoglobulin kappa constant	SEQ ID No:186		
ANG	81	angiogenin, ribonuclease, rnase a family, 5		SEQ ID No:194	SEQ ID No:195
EFNA1	95	ephrin-a1		SEQ ID No:226	SEQ ID No:227
MYBL2	131	v-myb avian myeloblastosis viral oncogene homolog-like 2	SEQ ID No:308	SEQ ID No:309	SEQ ID No:310
CDH1	138	cadherin 1, type 1, e-cadherin (epithelial)	SEQ ID No:326	SEQ ID No:327	SEQ ID No:328
MST1	140	macrophage stimulating 1 (hepatocyte growth factor-like)	SEQ ID No:331	SEQ ID No:332	SEQ ID No:333
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
XPB1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
SRF	164	serum response factor (c-fos serum response element-binding transcription factor)	SEQ ID No:391	SEQ ID No:392	SEQ ID No:393
SOX9	165	sry (sex determining region y)-box 9 (campomelic dysplasia, autosomal sex-reversal)	SEQ ID No:394		SEQ ID No:395
ESTs H21879 & H21880	183	Homo sapiens plasminogen activator (PLAT)	SEQ ID No:433	SEQ ID No:434	

Tables 8A and 8B hereunder relate to two sub populations of polynucleotide sequences particularly interesting to distinguish tumors sensitive to antracycline from tumors unsensitive to antracycline.

TABLEAU 8A

overexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
KIAA1075	136	kiaa1075 protein	SEQ ID No:322	SEQ ID No:323	
MMP11	145	matrix metalloproteinase 11 (stromelysin 3)	SEQ ID No:345		SEQ ID No:346
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
GZMA	169	granzyme a (granzyme 1, cytotoxic t-lymphocyte-associated serine esterase 3)	SEQ ID No:402		SEQ ID No:403

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TABLEAU 8B

underexpressed genes : top 5

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
SOX4	11	sry (sex determining region y)-box 4	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
IL2RB	40	interleukin 2 receptor, beta	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
EGFR	57	epidermal growth factor receptor (avian erythroblastic leukemia viral (v-erb-b) oncogene homolog)	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
IL2RG	119	interleukin 2 receptor, gamma (severe combined immunodeficiency)	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
CD3G	174	cd3g antigen, gamma polypeptide (tit3 complex)	SEQ ID No:414	SEQ ID No:415	SEQ ID No:416

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Tables 9, 9A and 9B hereunder relates to sub populations of polynucleotide sequences particularly interesting in classifying good and poor prognosis primary breast tumors.

TABLE 9

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
CTSB	14	cathepsin b		SEQ ID No:30	SEQ ID No:31
VIL2	23	villin 2 (ezrin)	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
MUC1	25	mucin 1, transmembrane		SEQ ID No:57	SEQ ID No:58
EMR1	27	egf-like module containing, mucin-like, hormone receptor-like sequence 1	SEQ ID No:62	SEQ ID No:63	SEQ ID No:64
KIAA0427	28	kiaa0427 gene product	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
PRLR	39	prolactin receptor	SEQ ID No:94	SEQ ID No:95	SEQ ID No:96
GATA3	41	gata-binding protein 3	SEQ ID No:100	SEQ ID No:101	SEQ ID No:78
TC21	44	oncogene tc21	SEQ ID No:106	SEQ ID No:107	SEQ ID No:108
BCL2	48	b-cell cll/lymphoma 2	SEQ ID No:115	SEQ ID No:116	SEQ ID No:117
GATA3	51	gata-binding protein 3	SEQ ID No:122		SEQ ID No:78
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
ANG	81	angiogenin, ribonuclease, rnase a family, 5		SEQ ID No:194	SEQ ID No:195
EGF	83	epidermal growth factor (beta-urogastrone)	SEQ ID No:199		SEQ ID No:200
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
EDNRA	96	endothelin receptor type a	SEQ ID No:228		SEQ ID No:229
SMARCA2	99	swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	SEQ ID No:235	SEQ ID No:236	SEQ ID No:237
ABCB1	108	atp-binding cassette, subfamily b (mdr/tap), member 1	SEQ ID No:257		SEQ ID No:258
EGF	110	epidermal growth factor (beta-urogastrone)	SEQ ID No:262		SEQ ID No:200
BIRC4	116	baculoviral iap repeat-containing 4	SEQ ID No:273		SEQ ID No:274
DAP3	117	death associated protein 3	SEQ ID		SEQ ID

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
			No:275		No:276
GNRH1	118	gonadotropin-releasing hormone 1 (leutinizing-releasing hormone)		SEQ ID No:277	SEQ ID No:278
DAP3	120	death associated protein 3	SEQ ID No:282	SEQ ID No:283	SEQ ID No:276
EST R97218	126	ests, highly similar to tvhume hepatocyte growth factor receptor precursor [h.sapiens]	SEQ ID No:296	SEQ ID No:297	
BCL2	142	b-cell cll/lymphoma 2	SEQ ID No:337	SEQ ID No:338	SEQ ID No:117
BS69	144	adenovirus 5 ela binding protein	SEQ ID No:342	SEQ ID No:343	SEQ ID No:344
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
CTSB	152	cathepsin b	SEQ ID No:361		SEQ ID No:31
MLANA	153	melan-a	SEQ ID No:362	SEQ ID No:363	SEQ ID No:364
APR-1	154	apr-1 protein	SEQ ID No:365	SEQ ID No:366	SEQ ID No:367
TC21	157	oncogene tc21	SEQ ID No:372	SEQ ID No:373	SEQ ID No:108
CDKN3	159	cyclin-dependent kinase inhibitor 3 (cdk2-associated dual specificity phosphatase)	SEQ ID No:377	SEQ ID No:378	SEQ ID No:379
XBPI	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
CDH15	166	cadherin 15, m-cadherin (myotubule)	SEQ ID No:396	SEQ ID No:397	SEQ ID No:398
BCL2	167	b-cell cll/lymphoma 2	SEQ ID No:399	SEQ ID No:400	SEQ ID No:117
EST W73386	168	ests	SEQ ID No:401		
ILF1	171	interleukin enhancer binding factor 1	SEQ ID No:406	SEQ ID No:407	SEQ ID No:408
ARHGDIA	172	rho gdp dissociation inhibitor (gdi) alpha	SEQ ID No:409	SEQ ID No:410	SEQ ID No:411
C4A	173	complement component 4a	SEQ ID No:412		SEQ ID No:413
ESR1	176	estrogen receptor 1	SEQ ID No:420	SEQ ID No:421	SEQ ID No:422
PBX1	177	pre-b-cell leukemia transcription factor 1	SEQ ID No:423	SEQ ID No:424	SEQ ID No:425
GLI3	178	gli-kruppel family member gli3 (greig	SEQ ID No:426	SEQ ID No:427	SEQ ID No:428

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
		cephalopolysyndactyly syndrome)			
ILF1	179	interleukin enhancer binding factor 1	SEQ ID No:429		SEQ ID No:408
ESTs H24628 & H24592	184	Homo sapiens aminoacylase 1 (ACY1).	SEQ ID No:435	SEQ ID No:436	
EST H28056	185	Homo sapiens E74-like factor 1 (ets domain transcription factor) (ELF1)	SEQ ID No:437		

**TABLE 9A**

Gene symbol	SET N°	Name	Seq3'	Seq5'	Ref
VIL2	23	villin 2 (ezrin)	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
MUC1	25	mucin 1, transmembrane		SEQ ID No:57	SEQ ID No:58
GATA3	32	gata-binding protein 3	SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
GATA3	41	gata-binding protein 3	SEQ ID No:100	SEQ ID No:101	SEQ ID No:78
BCL2	48	b-cell cll/lymphoma 2	SEQ ID No:115	SEQ ID No:116	SEQ ID No:117
GATA3	51	gata-binding protein 3	SEQ ID No:122		SEQ ID No:78
CRABP2	64	cellular retinoic acid-binding protein 2	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
ANG	81	angiogenin, ribonuclease, rnase a family, 5		SEQ ID No:194	SEQ ID No:195
EGF	83	epidermal growth factor (beta-urogastrone)	SEQ ID No:199		SEQ ID No:200
THBS1	91	thrombospondin 1	SEQ ID No:216		SEQ ID No:217
SMARCA2	99	swi/snf related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	SEQ ID No:235	SEQ ID No:236	SEQ ID No:237
EGF	110	epidermal growth factor (beta-urogastrone)	SEQ ID No:262		SEQ ID No:200
BIRC4	116	baculoviral iap repeat-containing 4	SEQ ID No:273		SEQ ID No:274
BCL2	142	b-cell cll/lymphoma 2	SEQ ID No:337	SEQ ID No:338	SEQ ID No:117



Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
BS69	144	adenovirus 5 ela binding protein	SEQ ID No:342	SEQ ID No:343	SEQ ID No:344
MYB	149	v-myb avian myeloblastosis viral oncogene homolog		SEQ ID No:354	SEQ ID No:355
XBP1	162	x-box binding protein 1	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
BCL2	167	b-cell cll/lymphoma 2	SEQ ID No:399	SEQ ID No:400	SEQ ID No:117
ILF1	171	interleukin enhancer binding factor 1	SEQ ID No:406	SEQ ID No:407	SEQ ID No:408
ARHGDIA	172	rho gdp dissociation inhibitor (gdi) alpha	SEQ ID No:409	SEQ ID No:410	SEQ ID No:411
C4A	173	complement component 4a	SEQ ID No:412		SEQ ID No:413
ESR1	176	estrogen receptor 1	SEQ ID No:420	SEQ ID No:421	SEQ ID No:422
PBX1	177	pre-b-cell leukemia transcription factor 1	SEQ ID No:423	SEQ ID No:424	SEQ ID No:425
GLI3	178	gli-kruppel family member gli3 (greig cephalopolysyndactyly syndrome)	SEQ ID No:426	SEQ ID No:427	SEQ ID No:428
ILF1	179	interleukin enhancer binding factor 1	SEQ ID No:429		SEQ ID No:408
ESTs H24628 & H24592	184	Homo sapiens aminoacylase 1 (ACY1).	SEQ ID No:435	SEQ ID No:436	
EST H28056	185	Homo sapiens E74-like factor 1 (ets domain transcription factor) (ELF1)	SEQ ID No:437		

TABLE 9B

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
CTSB	14	cathepsin b		SEQ ID No:30	SEQ ID No:31
EMR1	27	egf-like module containing, mucin-like, hormone receptor-like sequence 1	SEQ ID No:62	SEQ ID No:63	SEQ ID No:64
KIAA0427	28	kiaa0427 gene product	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
PRLR	39	prolactin receptor	SEQ ID No:94	SEQ ID No:95	SEQ ID No:96
TC21	44	oncogene tc21	SEQ ID No:106	SEQ ID No:107	SEQ ID No:108

Gene symbol	SET No	Name	Seq3'	Seq5'	Ref
EDNRA	96	endothelin receptor type a	SEQ ID No:228		SEQ ID No:229
ABCB1	108	atp-binding cassette, sub-family b (mdr/tap), member 1	SEQ ID No:257		SEQ ID No:258
DAP3	117	death associated protein 3	SEQ ID No:275		SEQ ID No:276
GNRH1	118	gonadotropin-releasing hormone 1 (leutinizing-releasing hormone)		SEQ ID No:277	SEQ ID No:278
DAP3	120	death associated protein 3	SEQ ID No:282	SEQ ID No:283	SEQ ID No:276
EST R97218	126	ests, highly similar to tvhume hepatocyte growth factor receptor precursor [h.sapiens]	SEQ ID No:296	SEQ ID No:297	
CTSB	152	cathepsin b	SEQ ID No:361		SEQ ID No:31
MLANA	153	melan-a	SEQ ID No:362	SEQ ID No:363	SEQ ID No:364
APR-1	154	apr-1 protein	SEQ ID No:365	SEQ ID No:366	SEQ ID No:367
TC21	157	oncogene tc21	SEQ ID No:372	SEQ ID No:373	SEQ ID No:108
CDKN3	159	cyclin-dependent kinase inhibitor 3 (cdk2-associated dual specificity phosphatase)	SEQ ID No:377	SEQ ID No:378	SEQ ID No:379
CDH15	166	cadherin 15, m-cadherin (myotubule)	SEQ ID No:396	SEQ ID No:397	SEQ ID No:398
EST W73386	168	ests	SEQ ID No:401		

Overexpression of genes detected by using at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences indicated in table 9A combined with underexpression of genes detected with at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequence indicated on table 9B present a Good outcome.

So, a preferred DNA array according to the invention comprises at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences indicated in table 9A and at least

one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequence indicated on table 9B.

5           Such DNA arrays are particularly useful to distinguish patients having a high risk (Bad Outcome) from those having a good pronostic (Good Outcome).

TABLE 10

CORRELATION BETWEEN SEQ ID NO AS FILED WITH US PROVISIONAL APPLICATION N° 60/254,090  
and SEQ ID NO FILED WITH PCT APPLICATION

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
GATA3	1	GATA-binding protein 3 (GATA3)	129757	SEQ ID No : 1		SEQ ID No:76	SEQ ID No:77	SEQ ID No:78
MYB	2	v-myb avian myeloblastosis viral oncogene homolog (MYB)	248613		SEQ ID No : 2	0	SEQ ID No:354	SEQ ID No:355
KIAA1075	3	KIAA1075 protein	211999	SEQ ID No : 3	SEQ ID No : 4	SEQ ID No:322	SEQ ID No:323	0
STMY3	4	matrix metalloproteinase 11 (stromelysin 3) (MMP11) (ex STMY3)	235947	SEQ ID No : 5		SEQ ID No:345	0	SEQ ID No:346
HGFL	5	macrophage-stimulating protein (MST1) (ex HGFL)	229839	SEQ ID No : 6	SEQ ID No : 7	SEQ ID No:331	SEQ ID No:332	SEQ ID No:333
CRABP	6	cellular retinoic acid-binding protein 2 (CRABP2)	153275	SEQ ID No : 8	SEQ ID No : 9	SEQ ID No:156	SEQ ID No:157	SEQ ID No:158
XBP1	7	X-box binding protein 1 (XBP1)	301950	SEQ ID No : 10	SEQ ID No : 11	SEQ ID No:385	SEQ ID No:386	SEQ ID No:387
TP53	8	tumor protein p53 (LI-Fraumeni syndrome) (TP53)	205314		SEQ ID No : 12	SEQ ID No:442	0	0
IGF2	9	insulin-like growth factor 2 (somatomedin A) (IGF2)	126233	SEQ ID No : 13	SEQ ID No : 14	SEQ ID No:59	SEQ ID No:60	SEQ ID No:61
CD3G	10	CD3G antigen, gamma polypeptide (TIT3 complex) (CD3G)	66322	SEQ ID No : 15	SEQ ID No : 16	SEQ ID No:414	SEQ ID No:415	SEQ ID No:418
IL2RG	11	interleukin 2 receptor, gamma (severe combined immunodeficiency) (IL2RG)	195022	SEQ ID No : 17	SEQ ID No : 18	SEQ ID No:279	SEQ ID No:280	SEQ ID No:281
SOX4	12	SRY (sex determining region Y)-box 4 (SOX4)	111461	SEQ ID No : 19	SEQ ID No : 20	SEQ ID No:22	SEQ ID No:23	SEQ ID No:24
EGFR	13	epidermal growth factor receptor (avian erythroblastic)	151475	SEQ ID No : 21	SEQ ID No : 22	SEQ ID No:135	SEQ ID No:136	SEQ ID No:137
TOP2B	14	topIIb mRNA for topoisomerase IIb.	130788		SEQ ID No : 23	0	SEQ ID No:82	SEQ ID No:83
S100B	15	S100 calcium-binding protein, beta (neural) (S100B)	183641		SEQ ID No : 24	0	SEQ ID No:255	SEQ ID No:256
EST N53133	16	EST N53133	246820	SEQ ID No : 25		SEQ ID No:352	0	SEQ ID No:353
GSTP1	17	glutathione S-transferase pl (GSTP1)	231424	SEQ ID No : 26	SEQ ID No : 27	SEQ ID No:334	SEQ ID No:335	SEQ ID No:336
THBS1	18	thrombospondin 1 (THBS1)	160963	SEQ ID No : 28		SEQ ID No:216	0	SEQ ID No:217

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
PDP2	19	actonucleotide pyrophosphatase/phosphodiesterase 2 (autotaxin) (ENPP2) (ex PDNP2)	120916	SEQ ID No : 29	SEQ ID No : 30	SEQ ID No:39	SEQ ID No:40	SEQ ID No:41
ATF3	20	activating transcription factor 3 (ATF3)	183030	SEQ ID No : 31	SEQ ID No : 32	SEQ ID No:250	SEQ ID No:251	SEQ ID No:252
NF1A	21	(ex NF1A)	110480	SEQ ID No : 33		SEQ ID No:16	0	0
SELP	22	selectin P (granule membrane protein 140kD, antigen CD62) (SELP)	182264		SEQ ID No : 34	SEQ ID No:438	SEQ ID No:439	0
CDH1	23	cadherin 1, E-cadherin (epithelial) (CDH1)	214008	SEQ ID No : 35	SEQ ID No : 36	SEQ ID No:326	SEQ ID No:327	SEQ ID No:328
ERBB2	24	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 2 (neuro/glioblastoma derived oncogene homolog) (ERBB2)	147016	SEQ ID No : 37		0	SEQ ID No:118	SEQ ID No:119
PP2A BR gamma	25	(PP2A BR gamma)	179197	SEQ ID No : 38	SEQ ID No : 39	SEQ ID No:238	SEQ ID No:239	0
ZNF144	26	zinc finger protein 144 (Mel-18) (ZNF144)	220451	SEQ ID No : 40	SEQ ID No : 41	0	SEQ ID No:329	SEQ ID No:330
MUC1	27	mucin 1, transmembrane (MUC1)	125413		SEQ ID No : 42	0	SEQ ID No:57	SEQ ID No:58
CD44	28	CD44E (epithelial form)	290007	SEQ ID No : 43	SEQ ID No : 44	SEQ ID No:374	SEQ ID No:375	SEQ ID No:376
PLA2G2A	29	phospholipase A2, group IIA (platelets, synovial fluid) (PLA2G2A), nuclear gene encoding mitochondrial protein	152802	SEQ ID No : 45	SEQ ID No : 46	SEQ ID No:147	SEQ ID No:148	SEQ ID No:149
ACVRL1	30	activin A receptor type II-like 1 (ACVRL1)	153350	SEQ ID No : 47	SEQ ID No : 48	SEQ ID No:159	SEQ ID No:160	SEQ ID No:161
AXL	31	AXL receptor tyrosine kinase (AXL)	112500	SEQ ID No : 49	SEQ ID No : 50	SEQ ID No:27	SEQ ID No:28	SEQ ID No:29
PKU-ALPHA	32	KU-alpha, partial cds (new gene symbol Ttk2)	109569		SEQ ID No : 51	0	SEQ ID No:5	SEQ ID No:6
ABCC5	33	ATP-binding cassette, sub-family C (CFTR/MRP), member 5 (ABCC5)	212366		SEQ ID No : 52	0	SEQ ID No:324	SEQ ID No:325
EDNRB	34	endothelin receptor type B (EDNRB), transcript variant1	154244		SEQ ID No : 53	0	SEQ ID No:176	SEQ ID No:177
DTR	35	diphtheria toxin receptor (heparin-binding epidermal)	187547		SEQ ID No : 54	0	SEQ ID No:265	SEQ ID No:266
IGF1R	36	insulin-like growth factor 1 receptor (IGF1R)	150361		SEQ ID No : 55	0	SEQ ID No:129	SEQ ID No:130
KIAA0427	37	KIAA0427	127507	SEQ ID No : 56	SEQ ID No : 57	SEQ ID No:65	SEQ ID No:66	SEQ ID No:67
CD69	38	CD69 antigen (p60, early T-cell activation antigen)	276727		SEQ ID No : 58	0	SEQ ID No:370	SEQ ID No:371
FGFR4	39	fibroblast growth factor receptor 4 (FGFR4)	116781	SEQ ID No : 59	SEQ ID No : 60	SEQ ID No:36	SEQ ID No:37	SEQ ID No:38
EST T85683	40	EST T85683 cathepsin B (CTSB)	112822		SEQ ID No : 61	0	SEQ ID No:30	SEQ ID No:31
EST R00569	41	EST R00569 IL2-inducible T-cell kinase (ITK)	123871		SEQ ID No : 62	0	SEQ ID No:44	SEQ ID No:45

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
TGFB3	42	transforming growth factor, beta receptor III (TGFB3)	208118	SEQ ID No : 63	SEQ ID No : 64	SEQ ID No:311	SEQ ID No:312	SEQ ID No:313
INSR	43	insulin receptor (INSR)	151149		SEQ ID No : 65	0	SEQ ID No:131	SEQ ID No:132
MARK3	44	MAP/microtubule affinity-regulating kinase 3 (MARK3)	110599	SEQ ID No : 66	SEQ ID No : 67	#N/A	#N/A	#N/A
TIMP2	45	tissue inhibitor of metalloproteinase 2 (TIMP2)	131504		SEQ ID No : 68	0	SEQ ID No:86	SEQ ID No:87
EST R85557	46	EST R85557 thrombospondin 3 (THBS3)	180219	SEQ ID No : 69		SEQ ID No:240	0	SEQ ID No:241
GNRH1	47	gonadotropin-releasing hormone 1 (GNRH1)	192888		SEQ ID No : 70	0	SEQ ID No:277	SEQ ID No:278
FGFR2	48	fibroblast growth factor receptor 2 (FGFR2)	110387	SEQ ID No : 71	SEQ ID No : 72	SEQ ID No:13	SEQ ID No:14	SEQ ID No:15
NFKB2	49	NFKB2	114879	SEQ ID No : 73		SEQ ID No:35	0	0
VIL2	50	villin 2 (ezrin) (VIL2)	124701	SEQ ID No : 74	SEQ ID No : 75	SEQ ID No:51	SEQ ID No:52	SEQ ID No:53
ENG	51	endoglin (ENG)	156979	SEQ ID No : 76	SEQ ID No : 77	SEQ ID No:196	SEQ ID No:197	SEQ ID No:198
EPHA2	52	Epha2 (EPHA2)	162004	SEQ ID No : 78		SEQ ID No:221	0	SEQ ID No:222
CREM	53	CAMP responsive element modulator (CREM)	258584	SEQ ID No : 79	SEQ ID No : 80	SEQ ID No:358	SEQ ID No:359	SEQ ID No:360
ETV5-a	54	ets variant gene 5 (ETV5)	270549	SEQ ID No : 81	SEQ ID No : 82	SEQ ID No:368	SEQ ID No:369	SEQ ID No:300
EST N68536	55	EST N68536 MAX-interacting protein 1 (MXI1)	298242	SEQ ID No : 83	SEQ ID No : 84	0	SEQ ID No:380	SEQ ID No:381
EST R81126	56	EST R81126 lymphotoxin beta receptor (LTBR)	146635	SEQ ID No : 85	SEQ ID No : 86	SEQ ID No:114	0	0
POU2F2	57	(POU2F2)	188393	SEQ ID No : 87	SEQ ID No : 88	SEQ ID No:271	0	SEQ ID No:272
FLI1	58	Friend leukemia virus integration 1 (FLI1)	198144	SEQ ID No : 89	SEQ ID No : 90	SEQ ID No:293	SEQ ID No:294	SEQ ID No:295
TIE	59	tyrosine kinase with immunoglobulin and epidermal growth factor homology domains (TIE)	144081		SEQ ID No : 91	0	SEQ ID No:109	SEQ ID No:110
PRLR	60	prolactin receptor (PRLR)	138788	SEQ ID No : 92	SEQ ID No : 93	SEQ ID No:94	SEQ ID No:95	SEQ ID No:96
PPP3CA	61	protein phosphatase 3 (formerly 2B), catalytic subunit, gamma isoform (calcineurin A gamma) (PPP3CC) (ex PPP3CA)	110481	SEQ ID No : 94	SEQ ID No : 95	SEQ ID No:17	SEQ ID No:18	SEQ ID No:19
PTPN2	62	protein tyrosine phosphatase, non-receptor type 2 (PTPN2)	161451	SEQ ID No : 96	SEQ ID No : 97	SEQ ID No:218	SEQ ID No:219	SEQ ID No:220
PGF	63	placental growth factor, vascular endothelial growth factor-related protein (PGF)	138326		SEQ ID No : 98	0	SEQ ID No:102	SEQ ID No:103
TNFAIP3	64	tumor necrosis factor, alpha-induced	305943	SEQ ID No : 99		SEQ ID No:388	SEQ ID No:389	SEQ ID No:390

Symbol gene	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
		protein 3 (TNFAIP3)						
PHB	65	PHB (prohibitin)	236008	SEQ ID No : 100		SEQ ID No:347	SEQ ID No:348	SEQ ID No:349
RIL	66	LIM domain protein (RIL)	153446		SEQ ID No : 101	0	SEQ ID No:162	SEQ ID No:163
MYBL2	67	v-myb avian myeloblastosis viral oncogene homolog-like 2 (MYBL2)	207378	SEQ ID No : 102	SEQ ID No : 103	SEQ ID No:308	SEQ ID No:309	SEQ ID No:310
RELB	68	v-rel avian reticuloendotheliosis viral oncogene homolog B (nuclear factor of kappa light polypeptide gene enhancer in B-cells 3) (RELB)	66969	SEQ ID No : 104	SEQ ID No : 105	SEQ ID No:417	SEQ ID No:418	SEQ ID No:419
EST R97218	69	Est R97218	200394	SEQ ID No : 106		SEQ ID No:296	SEQ ID No:297	0
GZMH	70	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1) (GZMB) (ex GZMH)	154343	SEQ ID No : 107		SEQ ID No:178	0	SEQ ID No:179
MYC	71	c-myc proto-oncogene	129438	SEQ ID No : 108	SEQ ID No : 109	SEQ ID No:73	SEQ ID No:74	SEQ ID No:75
CASP1	72	caspase 4, apoptosis-related cysteine protease (CASP4) (ex CASP1)	131502		SEQ ID No : 110	SEQ ID No:84	0	SEQ ID No:85
SYK	73	spleen tyrosine kinase (SYK)	128142	SEQ ID No : 111	SEQ ID No : 112	SEQ ID No:68	SEQ ID No:69	SEQ ID No:70
EST H27202	74	EST H27202 transcription factor E1AF gene	158347	SEQ ID No : 113	SEQ ID No : 114	SEQ ID No:204	SEQ ID No:205	0
HRB	75	syndecan 1 (SDC1) (ex HRB)	108490	SEQ ID No : 115	SEQ ID No : 116	SEQ ID No:1	0	SEQ ID No:2
SHC1	76	p66shc (SHC)	153548		SEQ ID No : 117	0	SEQ ID No:164	SEQ ID No:165
CSF1	77	colony stimulating factor 1 (CSF1)	124554	SEQ ID No : 118	SEQ ID No : 119	SEQ ID No:48	SEQ ID No:49	SEQ ID No:50
UBE3A	78	ubiquitin protein ligase E3A (UBE3A)	141824		SEQ ID No : 120	0	SEQ ID No:104	SEQ ID No:105
FKHR	79	forkhead box O1A (rhabdomyosarcoma) (FOXO1A) (ex FKHR)	151247		SEQ ID No : 121	0	SEQ ID No:133	SEQ ID No:134
CSF1R	80	colony stimulating factor 1 receptor (CSF1R)	198282	SEQ ID No : 122		SEQ ID No:291	0	SEQ ID No:292
IFI75	81	interferon-induced protein 75 (IFI75)	205612	SEQ ID No : 123	SEQ ID No : 124	SEQ ID No:305	SEQ ID No:306	SEQ ID No:307
GATA1	82	GATA-binding protein 1 (globin transcription factor 1) (GATA1)	109093		SEQ ID No : 125	0	SEQ ID No:3	SEQ ID No:4
STAT1	83	signal transducer and activator of transcription 1 (STAT1)	110101		SEQ ID No : 126	0	SEQ ID No:11	SEQ ID No:12
CREBBP	84	CREB binding protein (Rubinstein-Taybi syndrome) (CREBBP)	109677	SEQ ID No : 127	SEQ ID No : 128	SEQ ID No:7	SEQ ID No:8	0
IL7R	85	interleukin 7 receptor (IL7R)	129059		SEQ ID No : 129	0	SEQ ID No:71	SEQ ID No:72
ANXA7	86	annexin A7 (ANXA7)	160580		SEQ ID No : 130	0	SEQ ID No:214	SEQ ID No:215

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
TNXA	87	tenascin XA (TNXA)	124340		SEQ ID No : 131	0	SEQ ID No:46	SEQ ID No:47
CNBP1	88	zinc finger protein 9 (a cellular retroviral nucleic acid binding protein) (ZNF9) (ex CNBP1)	251963	SEQ ID No : 132		SEQ ID No:356	0	SEQ ID No:357
CDK4-a	89	cyclin-dependent kinase 4 (CDK4)	204586	SEQ ID No : 133	SEQ ID No : 134	SEQ ID No:301	SEQ ID No:302	SEQ ID No:288
CSNK2B	90	gene for casein kinase II subunit beta (EC 2.7.1.37)	153879		SEQ ID No : 135	0	SEQ ID No:171	SEQ ID No:172
EFNA1	91	ephrin-A1 (EFNA1)	162997		SEQ ID No : 136	0	SEQ ID No:226	SEQ ID No:227
SELE	92	selectin E (endothelial adhesion molecule 1) (SELE)	186132	SEQ ID No : 137	SEQ ID No : 138	SEQ ID No:259	SEQ ID No:260	SEQ ID No:261
APC	93	adenomatosis polyposis coli (APC)	125294	SEQ ID No : 139	SEQ ID No : 140	SEQ ID No:54	SEQ ID No:55	SEQ ID No:56
FAK	94	PTK2 protein tyrosine kinase 2 (PTK2) (ex FAK)	195731		SEQ ID No : 141	0	SEQ ID No:284	SEQ ID No:285
FOS-a	95	v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS)	208717		SEQ ID No : 142	0	SEQ ID No:317	SEQ ID No:318
FGFR1	96	fibroblast growth factor receptor (FGFR)	154472	SEQ ID No : 143	SEQ ID No : 144	SEQ ID No:180	SEQ ID No:181	SEQ ID No:182
MC1R	97	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor) (MC1R)	155691		SEQ ID No : 145	0	SEQ ID No:187	SEQ ID No:188
PCNA	98	proliferating cell nuclear antigen (PCNA)	232941	SEQ ID No : 146	SEQ ID No : 147	SEQ ID No:339	SEQ ID No:340	SEQ ID No:341
DDT	99	D-dopachrome tautomerase (DDT)	132109	SEQ ID No : 148	SEQ ID No : 149	SEQ ID No:88	SEQ ID No:89	SEQ ID No:90
GRB2	100	growth factor receptor-bound protein 2 (GRB2)	172152	SEQ ID No : 150	SEQ ID No : 151	SEQ ID No:230	SEQ ID No:231	SEQ ID No:232
AMFR	101	autocrine motility factor receptor (AMFR)	146280	SEQ ID No : 152	SEQ ID No : 153	SEQ ID No:111	SEQ ID No:112	SEQ ID No:113
ITGB2	102	integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit) (ITGB2)	187822	SEQ ID No : 154		0	SEQ ID No:267	SEQ ID No:268
JUND	103	jun D proto-oncogene (JUND)	175421	SEQ ID No : 155		SEQ ID No:233	0	SEQ ID No:234
NF45	104	interleukin enhancer binding factor 2 (ILF2) (ex NF45)	243907		SEQ ID No : 156	0	SEQ ID No:350	SEQ ID No:351
PPP4C	105	protein phosphatase 4 (formerly X) (PPP4C)	114097	SEQ ID No : 157	SEQ ID No : 158	SEQ ID No:32	SEQ ID No:33	SEQ ID No:34
EMS1	106	ATX1 (antioxidant protein 1, yeast) homolog 1 (ATOX1)(ex EMS1)	149172	SEQ ID No : 159		SEQ ID No:123	SEQ ID No:124	SEQ ID No:125
BCL2	107	B-cell CLL/lymphoma 2 (BCL2), nuclear gene encoding mitochondrial protein, transcript variant alpha	147002	SEQ ID No : 160	SEQ ID No : 161	SEQ ID No:115	SEQ ID No:116	SEQ ID No:117
MGST1	108	protein phosphatase 1, catalytic subunit,	182610	SEQ ID No : 162	SEQ ID No : 163	SEQ ID No:248	0	SEQ ID No:249



Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
		alpha isoform (PPP1CA) (ex MGST1)						
PDGFRB	109	platelet-derived growth factor receptor, beta polypeptide (PDGFRB)	158976		SEQ ID No : 164	0	SEQ ID No:208	SEQ ID No:209
ANXA11	110	annexin A11 (ANXA11)	158892		SEQ ID No : 165	0	SEQ ID No:206	SEQ ID No:207
GPX1	111	histocompatibility class II antigen gamma chain (CD74) (ex GPX1 Glutathion S transférase)	159809		SEQ ID No : 166	0	SEQ ID No:212	SEQ ID No:213
CFR-1	112	Golgi apparatus protein 1 (GLG1) (ex CFR-1)	153974	SEQ ID No : 167	SEQ ID No : 168	SEQ ID No:173	SEQ ID No:174	SEQ ID No:175
BTF3L3	113	basic transcription factor 3 (BTF3)	195889	SEQ ID No : 169		SEQ ID No:289	0	SEQ ID No:290
EST R55460	114	EST R55460	154997		SEQ ID No : 170	0	SEQ ID No:185	0
AKT2	115	v-akt murine thymoma viral oncogene homolog 2 (AKT2)	183552	SEQ ID No : 171		SEQ ID No:253	0	SEQ ID No:254
CDKN1A	116	cyclin-dependent kinase inhibitor (CDKN1A)	152524	SEQ ID No : 172	SEQ ID No : 173	SEQ ID No:144	SEQ ID No:145	SEQ ID No:146
PPP2CA	117	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform (PPP2CA)	154685	SEQ ID No : 174	SEQ ID No : 175	0	SEQ ID No:183	SEQ ID No:184
MDM2	118	mouse double minute 2, human homolog of p53-binding protein (MDM2), transcript variant MDM2	148052	SEQ ID No : 176		0	SEQ ID No:120	SEQ ID No:121
TNFRSF6	119	tumor necrosis factor receptor superfamily, member 6 (TNFRSF6)	151767	SEQ ID No : 177	SEQ ID No : 178	SEQ ID No:141	SEQ ID No:142	SEQ ID No:143
CNTFR	120	ciliary neurotrophic factor receptor (CNTFR)	156431		SEQ ID No : 179	0	SEQ ID No:192	SEQ ID No:193
JUNB	121	jun B proto-oncogene (JUNB)	153213	SEQ ID No : 180	SEQ ID No : 181	SEQ ID No:153	SEQ ID No:154	SEQ ID No:155
CCND1	122	cyclin D1 (PRAD1; parathyroid adenomatosis 1) (CCND1)	110022	SEQ ID No : 182		SEQ ID No:9	0	SEQ ID No:10
TDPX1	123	peroxiredoxin 2 (PRDX2) (ex TDPX1)	208439	SEQ ID No : 183	SEQ ID No : 184	SEQ ID No:314	SEQ ID No:315	SEQ ID No:316
GRB7	124	growth factor receptor-bound protein 7 (GRB7)	130323	SEQ ID No : 185	SEQ ID No : 186	SEQ ID No:79	SEQ ID No:80	SEQ ID No:81
RBBP7	125	retinoblastoma-binding protein 7 (RBBP7)	210874	SEQ ID No : 187	SEQ ID No : 188	SEQ ID No:319	SEQ ID No:320	SEQ ID No:321
TIMP1	126	inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor) (TIMP1)	162246	SEQ ID No : 189	SEQ ID No : 190	SEQ ID No:223	SEQ ID No:224	SEQ ID No:225
YES1	127	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1 (YES1)	204634	SEQ ID No : 191		SEQ ID No:303	0	SEQ ID No:304
RNF5	128	ring finger protein 5 (RNF5)	112098		SEQ ID No : 192	0	SEQ ID No:25	SEQ ID No:26
PRKCSH	129	protein kinase C substrate 80K-H (PRKCSH)	187232		SEQ ID No : 193	0	SEQ ID No:263	SEQ ID No:264

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
CTSD	130	cathepsin D (lysosomal aspartyl protease) (CTSD)	149401	SEQ ID No : 194	SEQ ID No : 195	SEQ ID No:126	SEQ ID No:127	SEQ ID No:128
NEO1	131	neogenin (chicken) homolog 1 (NEO1)	188380		SEQ ID No : 196	0	SEQ ID No:269	SEQ ID No:270
GAPD-a	132	glyceraldehyde-3-phosphate dehydrogenase (GAPD)	152847	SEQ ID No : 197		SEQ ID No:150	SEQ ID No:151	SEQ ID No:152
ACTG1	133	actin, gamma 1 (ACTG1)	182291	SEQ ID No : 198	SEQ ID No : 199	SEQ ID No:242	SEQ ID No:243	SEQ ID No:244
ITGA6	134	integrin, alpha 6 (ITGA6)	182431	SEQ ID No : 200	SEQ ID No : 201	SEQ ID No:245	SEQ ID No:246	SEQ ID No:247
GAPD-b	135	glyceraldehyde-3-phosphate dehydrogenase (GAPD)	153607	SEQ ID No : 202	SEQ ID No : 203	SEQ ID No:166	SEQ ID No:167	SEQ ID No:168
ETV5-b	136	ets variant gene 5 (ets-related molecule) (ETV5)	203394	SEQ ID No : 204	SEQ ID No : 205	SEQ ID No:298	SEQ ID No:299	SEQ ID No:300
CDK4-b	137	cyclin-dependent kinase 4 (CDK4)	195800	SEQ ID No : 206	SEQ ID No : 207	SEQ ID No:286	SEQ ID No:287	SEQ ID No:288
FOS-b	138	v-fos FBJ murine osteosarcoma viral oncogene homolog (FOS)	363796	SEQ ID No : 208	SEQ ID No : 209	SEQ ID No:404	SEQ ID No:405	SEQ ID No:406
HOXA5	139	homeobox protein (HOX-1.3) (ex Hox A5)	300564	SEQ ID No : 210	SEQ ID No : 211	SEQ ID No:382	SEQ ID No:383	SEQ ID No:384
RELA	140	NF-kappa-B transcription factor p65 DNA binding subunit (ex RELa)	122056	SEQ ID No : 212		SEQ ID No:42	0	SEQ ID No:43
SUI1	141	S100 calcium-binding protein A11 (calgizarin) (S100A11)	155345	SEQ ID No : 213	SEQ ID No : 214	SEQ ID No:186	0	0
ANG	142	angiotensin, ribonuclease, RNase A family, 5 (ANG)	156720		SEQ ID No : 215	0	SEQ ID No:194	SEQ ID No:195
ITGA6	143	integrin, alpha 6 (ITGA6)	182431	SEQ ID No : 216	SEQ ID No : 217	SEQ ID No:245	SEQ ID No:246	SEQ ID No:247
PRMT2	144	HMT1 (hnRNP methyltransferase, S cerevisiae)-like 1 (HRMT1L1) (ex PRMT2)	158038	SEQ ID No : 218	SEQ ID No : 219	SEQ ID No:201	SEQ ID No:202	SEQ ID No:203
EST R55460	145	EST R55460	154997		SEQ ID No : 220	0	SEQ ID No:185	0
GZMA	146	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3) (GZMA)	356763	SEQ ID No : 221	SEQ ID No : 222	SEQ ID No:402	0	SEQ ID No:403
SOX9	147	SRY (sex-determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9)	323948	SEQ ID No : 223		SEQ ID No:394	0	SEQ ID No:395
SRF	148	serum response factor (c-fos serum response element-binding transcription factor) (SRF)	321329		SEQ ID No : 224	SEQ ID No:391	SEQ ID No:392	SEQ ID No:393
EDN1	149	endothelin 1 (EDN1)	153424	SEQ ID No : 225		#N/A	#N/A	#N/A
PTPN6	150	protein tyrosine phosphatase, non-receptor type 6 (PTPN6)	66778	SEQ ID No : 226		#N/A	#N/A	#N/A
TFAP4	151	transcription factor AP-4 (activating)	159093	SEQ ID No : 227		0	SEQ ID No:210	SEQ ID No:211

Symbole gène	N°	Nom	Image	Seq3' US PROV LISTING	Seq5' US PROV LISTING	Seq3' PCT Listing	Seq5' PCT Listing	(mRNA) PCT Listing
		enhancer binding protein 4) (TFAP4)						
ELF1	152	Human cis-acting sequence.Elf-1	182007	SEQ ID No : 228		SEQ ID No:437	0	0
CD2	153	CD2 antigen (p50), sheep red blood cell receptor (CD2)	120649	SEQ ID No : 229		SEQ ID No:431	0	0
CCND2	154	cyclin D2 (CCND2)	175256	SEQ ID No : 230		#N/A	#N/A	#N/A
IL3RA	155	Interleukin 3 receptor (hIL-3Ra)	183087	SEQ ID No : 231		SEQ ID No:440	SEQ ID No:441	0
JUP	156	junction plakoglobin (JUP)	157958	SEQ ID No : 232		#N/A	#N/A	#N/A
RBL2	157	retinoblastoma-like 2 (p130) (RBL2)	108571	SEQ ID No : 233		SEQ ID No:430	0	0
HOXA4	158	homeo box A4 (HOXA4)	110731	SEQ ID No : 234		SEQ ID No:20	SEQ ID No:21	0
ACY1	159	aminoacylase 1 (ACY1)	160764	SEQ ID No : 235		SEQ ID No:435	SEQ ID No:436	0
GADD45A	160	growth arrest and DNA-damage-inducible, alpha (GADD45A)	115176	SEQ ID No : 236		#N/A	#N/A	#N/A
nm23	161	non-metastatic cells 1, protein (NM23A) expressed in (NME1)	174388	SEQ ID No : 237		#N/A	#N/A	#N/A
BBC1	162	ribosomal protein L13 (RPL13) (ex BBC1)	178317	SEQ ID No : 238		#N/A	#N/A	#N/A
VEGFB	163	vascular endothelial growth factor B (VEGFB)	162499	SEQ ID No : 239		#N/A	#N/A	#N/A
LAMR1	164	laminin receptor 1 (67kD, ribosomal protein SA) (LAMR1)	199837	SEQ ID No : 240		#N/A	#N/A	#N/A
IL2RB	165	interleukin 2 receptor, beta (IL2RB)	139073	SEQ ID No : 241	SEQ ID No : 242	SEQ ID No:97	SEQ ID No:98	SEQ ID No:99
DES	166	desmin	153854	SEQ ID No : 243		SEQ ID No:168	SEQ ID No:169	SEQ ID No:170
PRL	167	prolactin	133738	SEQ ID No : 244		SEQ ID No:91	SEQ ID No:92	SEQ ID No:93
CSH1	168	Chorionic somatomammotropin hormone 1 (placental lactogen) = LACTOGEN Precursor	133891		SEQ ID No : 245	SEQ ID No:432	0	0
TEK	169	tyrosine protein kinase receptor	151501	SEQ ID No : 246	SEQ ID No : 247	SEQ ID No:138	SEQ ID No:139	SEQ ID No:140
Nrg1	170	neuregulin 1 (EST R72075)	155716	SEQ ID No : 248	SEQ ID No : 249	SEQ ID No:189	SEQ ID No:190	SEQ ID No:191
PLAT	rien	pas d'EST ni mRNA	160149			SEQ ID No:433	SEQ ID No:434	0
EST	rien		Image ?					
AW184517	rien							

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## CLAIMS

1. A polynucleotide library useful in the molecular characterization of a carcinoma, said library comprising a pool of polynucleotide sequences or subsequences thereof wherein said sequences or subsequences are either underexpressed or overpressed in tumor cells, further wherein said sequences or subsequences correspond substantially to any of the polynucleotide sequences set forth in any of SEQ ID Nos: 1 - 468 or the complement thereof.

2. A polynucleotide library according to Claim 1 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in anyone of the following predefined sets :

SET 1: (SEQ ID No:1; SEQ ID No:2); SET 2: (SEQ ID No:3; SEQ ID No:4); SET 3: (SEQ ID No:5; SEQ ID No:6); SET 4: (SEQ ID No:7; SEQ ID No:8); SET 5: (SEQ ID No:9; SEQ ID No:10); SET 6: (SEQ ID No:11; SEQ ID No:12); SET 7: (SEQ ID No:13; SEQ ID No:14; SEQ ID No:15); SET 8: (SEQ ID No:16); SET 9: (SEQ ID No:17; SEQ ID No:18; SEQ ID No:19); SET 10: (SEQ ID No:20; SEQ ID No:21); SET 11: (SEQ ID No:22; SEQ ID No:23; SEQ ID No:24); SET 12: (SEQ ID No:25; SEQ ID No:26); SET 13: (SEQ ID No:27; SEQ ID No:28; SEQ ID No:29); SET 14: (SEQ ID No:30; SEQ ID No:31); SET 15: (SEQ ID No:32; SEQ ID No:33; SEQ ID No:34) ; SET 16 : (SEQ ID No:35) ; SET 17 : (SEQ ID No:36; SEQ ID No:37; SEQ ID No:38) ; SET 18 : (SEQ ID No:39; SEQ ID No:40; SEQ ID No:41) ; SET 19 : (SEQ ID No:42; SEQ ID No:43) ; SET 20 : (SEQ ID No:44; SEQ ID No:45) ; SET 21 : (SEQ ID No:46; SEQ ID No:47) ; SET 22 : (SEQ ID No:48; SEQ ID No:49; SEQ ID No:50) ; SET 23 : (SEQ ID No:51; SEQ ID No:52; SEQ ID No:53) ; SET 24: (SEQ ID No:54; SEQ ID No:55; SEQ ID No:56) ; SET 25: (SEQ ID No:57; SEQ ID No:58) ; SET 26: (SEQ ID No:59; SEQ ID No:60; SEQ ID No:61) ; SET 27: (SEQ ID No:62; SEQ ID No:63; SEQ ID No:64) ; SET 28: (SEQ ID No:65; SEQ ID No:66; SEQ ID No:67) ;

SET 29: (SEQ ID No:68; SEQ ID No:69; SEQ ID No:70) ; SET 30: (SEQ ID No:71; SEQ ID No:72) ; SET 31 : (SEQ ID No:73; SEQ ID No:74; SEQ ID No:75) ; SET 32 : (SEQ ID No:76; SEQ ID No:77; SEQ ID No:78) ; SET 33 : (SEQ ID No:79; SEQ ID No:80; SEQ ID No:81) ; SET 34: (SEQ ID No:82; SEQ ID No:83) ; SET 35: (SEQ ID No:84; SEQ ID No:85) ; SET 36: (SEQ ID No:86; SEQ ID No:87) ; SET 37: (SEQ ID No:88; SEQ ID No:89; SEQ ID No:90) ; SET 38: (SEQ ID No:91; SEQ ID No:92; SEQ ID No:93) ; SET 39: (SEQ ID No:94; SEQ ID No:95; SEQ ID No:96) ; SET 40: (SEQ ID No:97; SEQ ID No:98; SEQ ID No:99) ; SET 41: (SEQ ID No:100; SEQ ID No:101; SEQ ID No:78) ; SET 42: (SEQ ID No:102; SEQ ID No:103) ; SET 43: (SEQ ID No:104; SEQ ID No:105) ; SET 44: (SEQ ID No:106; SEQ ID No:107; SEQ ID No:108) ; SET 45: (SEQ ID No:109; SEQ ID No:110) ; SET 46: (SEQ ID No:111; SEQ ID No:112; SEQ ID No:113) ; SET 47: (SEQ ID No:114) ; SET 48: (SEQ ID No:115; SEQ ID No:116; SEQ ID No:117) ; SET 49: (SEQ ID No:118; SEQ ID No:119) ; SET 50: (SEQ ID No:120; SEQ ID No:121) ; SET 51: (SEQ ID No:122; SEQ ID No:78) ; SET 52: (SEQ ID No:123; SEQ ID No:124; SEQ ID No:125) ; SET 53: (SEQ ID No:126; SEQ ID No:127; SEQ ID No:128) ; SET 54: (SEQ ID No:129; SEQ ID No:130) ; SET 55: (SEQ ID No:131; SEQ ID No:132) ; SET 56: (SEQ ID No:133; SEQ ID No:134) ; SET 57: (SEQ ID No:135; SEQ ID No:136; SEQ ID No:137) ; SET 58: (SEQ ID No:138; SEQ ID No:139; SEQ ID No:140) ; SET 59: (SEQ ID No:141; SEQ ID No:142; SEQ ID No:143) ; SET 60: (SEQ ID No:144; SEQ ID No:145; SEQ ID No:146) ; SET 61: (SEQ ID No:147; SEQ ID No:148; SEQ ID No:149) ; SET 62: (SEQ ID No:150; SEQ ID No:151; SEQ ID No:152) ; SET 63: (SEQ ID No:153; SEQ ID No:154; SEQ ID No:155) ; SET 64: (SEQ ID No:156; SEQ ID No:157; SEQ ID No:158) ; SET 65: (SEQ ID No:159; SEQ ID No:160; SEQ ID No:161) ; SET 66: (SEQ ID No:162; SEQ ID No:163) ; SET 67: (SEQ ID No:164; SEQ ID No:165) ; SET 68: (SEQ ID No:166; SEQ ID No:167; SEQ ID No:152) ; SET 69: (SEQ ID No:168; SEQ ID No:169; SEQ ID No:170) ; SET 70: (SEQ ID No:171; SEQ ID No:172) ; SET 71: (SEQ ID No:173; SEQ ID No:174; SEQ ID No:175) ; SET 72: (SEQ ID No:176; SEQ ID No:177) ; SET 73: (SEQ ID No:178; SEQ ID No:179) ; SET 74: (SEQ ID No:180; SEQ ID No:181; SEQ ID No:182) ; SET 75: (SEQ ID No:183; SEQ ID No:184) ; SET 76: (SEQ ID No:185) ; SET 77: (SEQ ID No:186) ; SET 78: (SEQ ID No:187; SEQ ID No:188) ; SET 79: (SEQ ID No:189;

SEQ ID No:190; SEQ ID No:191) ; SET 80: (SEQ ID No:192; SEQ ID No:193) ; SET 81: (SEQ ID No:194; SEQ ID No:195) ; SET 82: (SEQ ID No:196; SEQ ID No:197; SEQ ID No:198) ; SET 83: (SEQ ID No:199; SEQ ID No:200) ; SET 84: (SEQ ID No:201; SEQ ID No:202; SEQ ID No:203) ; SET 85: (SEQ ID No:204; SEQ ID No:205) ; SET 86: (SEQ ID No:206; SEQ ID No:207) ; SET 87: (SEQ ID No:208; SEQ ID No:209) ; SET 88: (SEQ ID No:210; SEQ ID No:211) ; SET 89: (SEQ ID No:212; SEQ ID No:213) ; SET 90: (SEQ ID No:214; SEQ ID No:215) ; SET 91: (SEQ ID No:216; SEQ ID No:217) ; SET 92: (SEQ ID No:218; SEQ ID No:219; SEQ ID No:220) ; SET 93: (SEQ ID No:221; SEQ ID No:222) ; SET 94: (SEQ ID No:223; SEQ ID No:224; SEQ ID No:225) ; SET 95: (SEQ ID No:226; SEQ ID No:227) ; SET 96: (SEQ ID No:228; SEQ ID No:229) ; SET 97: (SEQ ID No:230; SEQ ID No:231; SEQ ID No:232) ; SET 98: (SEQ ID No:233; SEQ ID No:234) ; SET 99: (SEQ ID No:235; SEQ ID No:236; SEQ ID No:237) ; SET 100: (SEQ ID No:238; SEQ ID No:239) ; SET 101: (SEQ ID No:240; SEQ ID No:241) ; SET 102: (SEQ ID No:242; SEQ ID No:243; SEQ ID No:244) ; SET 103: (SEQ ID No:245; SEQ ID No:246; SEQ ID No:247) ; SET 104: (SEQ ID No:248; SEQ ID No:249) ; SET 105: (SEQ ID No:250; SEQ ID No:251; SEQ ID No:252) ; SET 106: (SEQ ID No:253; SEQ ID No:254) ; SET 107: (SEQ ID No:255; SEQ ID No:256) ; SET 108: (SEQ ID No:257; SEQ ID No:258) ; SET 109: (SEQ ID No:259; SEQ ID No:260; SEQ ID No:261) ; SET 110: (SEQ ID No:262; SEQ ID No:263; SEQ ID No:264) ; SET 111: (SEQ ID No:265; SEQ ID No:266) ; SET 112: (SEQ ID No:267; SEQ ID No:268) ; SET 113: (SEQ ID No:269; SEQ ID No:270) ; SET 114: (SEQ ID No:271; SEQ ID No:272) ; SET 115: (SEQ ID No:273; SEQ ID No:274) ; SET 116: (SEQ ID No:275; SEQ ID No:276) ; SET 117: (SEQ ID No:277; SEQ ID No:278) ; SET 118: (SEQ ID No:279; SEQ ID No:280; SEQ ID No:281) ; SET 119: (SEQ ID No:282; SEQ ID No:283; SEQ ID No:284) ; SET 120: (SEQ ID No:285; SEQ ID No:286; SEQ ID No:287; SEQ ID No:288) ; SET 121: (SEQ ID No:289; SEQ ID No:290) ; SET 122: (SEQ ID No:291; SEQ ID No:292) ; SET 123: (SEQ ID No:293; SEQ ID No:294; SEQ ID No:295) ; SET 124: (SEQ ID No:296; SEQ ID No:297) ; SET 125: (SEQ ID No:298; SEQ ID No:299; SEQ ID No:300) ; SET 126: (SEQ ID No:301; SEQ ID No:302; SEQ ID No:303) ; SET 127: (SEQ ID No:304) ; SET 128: (SEQ ID No:288) ; SET 129: (SEQ ID No:305; SEQ ID No:306)

SEQ ID No:307) ; SET 131: (SEQ ID No:308; SEQ ID No:309; SEQ ID  
No:310) ; SET 132: (SEQ ID No:311; SEQ ID No:312; SEQ ID No:313) ;  
SET 133: (SEQ ID No:314; SEQ ID No:315; SEQ ID No:316) ; SET 134:  
(SEQ ID No:317; SEQ ID No:318) ; SET 135: (SEQ ID No:319; SEQ ID  
5 No:320; SEQ ID No:321) ; SET 136: (SEQ ID No:322; SEQ ID No:323) ;  
SET 137: (SEQ ID No:324; SEQ ID No:325) ; SET 138: (SEQ ID No:326;  
SEQ ID No:327; SEQ ID No:328) ; SET 139: (SEQ ID No:329; SEQ ID  
No:330) ; SET 140: (SEQ ID No:331; SEQ ID No:332; SEQ ID No:333) ;  
SET 141: (SEQ ID No:334; SEQ ID No:335; SEQ ID No:336) ; SET 142:  
10 (SEQ ID No:337; SEQ ID No:338; SEQ ID No:117) ; SET 143: (SEQ ID  
No:339; SEQ ID No:340; SEQ ID No:341) ; SET 144: (SEQ ID No:342;  
SEQ ID No:343; SEQ ID No:344) ; SET 145: (SEQ ID No:345; SEQ ID  
No:346) ; SET 146: (SEQ ID No:347; SEQ ID No:348; SEQ ID No:349) ;  
SET 147: (SEQ ID No:350; SEQ ID No:351) ; SET 148: (SEQ ID No:352;  
15 SEQ ID No:353) ; SET 149: (SEQ ID No:354; SEQ ID No:355) ; SET  
150: (SEQ ID No:356; SEQ ID No:357) ; SET 151: (SEQ ID No:358; SEQ  
ID No:359; SEQ ID No:360) ; SET 152: (SEQ ID No:361; SEQ ID No:31)  
; SET 153: (SEQ ID No:362; SEQ ID No:363; SEQ ID No:364) ; SET  
154: (SEQ ID No:365; SEQ ID No:366; SEQ ID No:367) ; SET 155: (SEQ  
20 ID No:368; SEQ ID No:369; SEQ ID No:300) ; SET 156: (SEQ ID  
No:370; SEQ ID No:371) ; SET 157: (SEQ ID No:372; SEQ ID No:373;  
SEQ ID No:108) ; SET 158: (SEQ ID No:374; SEQ ID No:375; SEQ ID  
No:376) ; SET 159: (SEQ ID No:377; SEQ ID No:378; SEQ ID No:379) ;  
SET 160: (SEQ ID No:380; SEQ ID No:381) ; SET 161: (SEQ ID No:382;  
25 SEQ ID No:383; SEQ ID No:384) ; SET 162: (SEQ ID No:385; SEQ ID  
No:386; SEQ ID No:387) ; SET 163: (SEQ ID No:388; SEQ ID No:389;  
SEQ ID No:390) ; SET 164: (SEQ ID No:391; SEQ ID No:392; SEQ ID  
No:393) ; SET 165: (SEQ ID No:394; SEQ ID No:395) ; SET 166: (SEQ  
ID No:396; SEQ ID No:397; SEQ ID No:398) ; SET 167: (SEQ ID  
30 No:399; SEQ ID No:400; SEQ ID No:117) ; SET 168: (SEQ ID No:401) ;  
SET 169: (SEQ ID No:402; SEQ ID No:403) ; SET 170: (SEQ ID No:404;  
SEQ ID No:405; SEQ ID No:318) ; SET 171: (SEQ ID No:406; SEQ ID  
No:407; SEQ ID No:408) ; SET 172: (SEQ ID No:409; SEQ ID No:410;  
SEQ ID No:411) ; SET 173: (SEQ ID No:412; SEQ ID No:413) ; SET  
35 174: (SEQ ID No:414; SEQ ID No:415; SEQ ID No:416) ; SET 175: (SEQ  
ID No:417; SEQ ID No:418; SEQ ID No:419) ; SET 176: (SEQ ID  
No:420; SEQ ID No:421; SEQ ID No:422) ; SET 177: (SEQ ID No:423;

SEQ ID No:424; SEQ ID No:425) ; SET 178: (SEQ ID No:426; SEQ ID No:427; SEQ ID No:428) ; SET 179: (SEQ ID No:429; SEQ ID No:408) ; SET 180: (SEQ ID No:430) ; SET 181: (SEQ ID No:431) ; SET 182: (SEQ ID No:432) ; SET 183: (SEQ ID No:433; SEQ ID No:434) ; SET 184: (SEQ ID No:435; SEQ ID No:436) ; SET 185: (SEQ ID No:437) ; SET 186: (SEQ ID No:438; SEQ ID No:439) ; SET 187: (SEQ ID No:440; SEQ ID No:441) ; SET 188: (SEQ ID No:442) ; SET 189: (SEQ ID No:444) ; SET 190: (SEQ ID No:445) ; SET 191 (SEQ ID No:446 ; SEQ ID No:447) ; SET 192: (SEQ ID No:448) ; SET 193: (SEQ ID No:449) ; SET 194: (SEQ ID No:450) ; SET 195: (SEQ ID No:451) ; SET 196: (SEQ ID No:452) ; SET 197: (SEQ ID No:453) ; SET 198: (SEQ ID No:454) ; SET 199: (SEQ ID No:455) ; SET 200: (SEQ ID No:456) ; SET 201: (SEQ ID No:457) ; SET 202: (SEQ ID No:458) ; SET 203: (SEQ ID No:459) ; SET 204: (SEQ ID No:460) ; SET 205: (SEQ ID No:461) ; SET 206: (SEQ ID No:462) ; SET 207: (SEQ ID No:463) ; SET 208: (SEQ ID No:464) ; SET 209: (SEQ ID No:465) ; SET 210: (SEQ ID No:466) ; SET 211: (SEQ ID No:467) ; SET 212: (SEQ ID No:468)

3. A polynucleotide library according to Claim 2 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

4. A library according to anyone Claim 1 or 2 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 1: (SEQ ID No:1 ; SEQ ID No:2) ; SET 4: (SEQ ID No:7 ; SEQ ID No:8) ; SET 18: (SEQ ID No:39 ; SEQ ID No:40 ; SEQ ID No:41) ; SET 21: (SEQ ID No:46 ; SEQ ID No:47) ; SET 24: (SEQ ID No:54 ; SEQ ID No:55 ; SEQ ID No:56) ; SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET 38: (SEQ ID No:91 ; SEQ ID

No:92 ; SEQ ID No:93) ; SET 48: (SEQ ID No:115 ; SEQ ID No:116 ;  
SEQ ID No:117) ; SET 53: (SEQ ID No:126 ; SEQ ID No:127 ; SEQ ID  
No:128) ; SET 58: (SEQ ID No:138 ; SEQ ID No:139 ; SEQ ID No:140)  
; SET 59: (SEQ ID No:141 ; SEQ ID No:142 ; SEQ ID No:143) ; SET  
5 61: (SEQ ID No:147 ; SEQ ID No:148 ; SEQ ID No:149) ; SET 64: (SEQ  
ID No:156 ; SEQ ID No:157 ; SEQ ID No:158) ; SET 66: (SEQ ID  
No:162 ; SEQ ID No:163) ; SET 69: (SEQ ID No:168 ; SEQ ID No:169;  
SEQ ID No:170) ; SET 73: (SEQ ID No:178; SEQ ID No:179) ; SET 85:  
(SEQ ID No:204; SEQ ID No:205) ; SET 88: (SEQ ID No:210; SEQ ID  
10 No:211) ; SET 91: (SEQ ID No:216; SEQ ID No:217) ; SET 97: (SEQ ID  
No:230; SEQ ID No:231; SEQ ID No:232) ; SET 104: (SEQ ID No:248;  
SEQ ID No:249) ; SET 105: (SEQ ID No:250 ; SEQ ID No:251 ; SEQ ID  
No:252) ; SET 112: (SEQ ID No:265 ; SEQ ID No:266) ; SET 113: (SEQ  
ID No:267 ; SEQ ID No:268) ; SET 115 ; (SEQ ID No:271 ; SEQ ID  
15 No:272) ; SET 131: (SEQ ID No:308 ; SEQ ID No:309 ; SEQ ID No:310)  
; SET 132: (SEQ ID No:311 ; SEQ ID No:312 ; SEQ ID No:313) ; SET  
134: (SEQ ID No:317 ; SEQ ID No:318) ; SET 137: (SEQ ID No:324 ;  
SEQ ID No:325) ; SET 145: (SEQ ID No:345 ; SEQ ID No:346) ; SET  
147: (SEQ ID No:350 ; SEQ ID No:351) ; SET 155: (SEQ ID No:368 ;  
20 SEQ ID No:369 ; SEQ ID No:300) ; SET 175: (SEQ ID No:417 ; SEQ ID  
No:418 ; SEQ ID No:419) ; SET 180: (SEQ ID No:430) ; SET 181: (SEQ  
ID No:431) ; SET 182: (SEQ ID No:432) ; SET 185: (SEQ ID No:437) ;  
SET 187: (SEQ ID No:440 ; SEQ ID No:441,

wherein said sequences are useful in  
25 differentiating a normal cell from a cancer cell.

5. A polynucleotide library according to Claim  
4 wherein said polynucleotide sequences or subsequences  
thereof of said pool correspond to any combination of at  
30 least one polynucleotide selected among those included in at  
least 50%, preferably 75% and more preferably 100% of the  
predefined sets.

6. A polynucleotide library according to Claim 4  
35 wherein the pool of polynucleotide sequences or subsequences



correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

5           SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78)  
; SET 73: (SEQ ID No:178 ; SEQ ID No:179) ; SET 131: (SEQ ID  
No:308 ; SEQ ID No:309 ; SEQ ID No:310) ; SET 145: (SEQ ID No:345  
; SEQ ID No:346) and SET 181: (SEQ ID No:431)

10           and of at least one polynucleotide sequence  
selected among those included in each one of predefined  
polynucleotide sequences sets comprising:

15           SET 38: (SEQ ID No:91 ; SEQ ID No:92 ; SEQ ID No:93)  
; SET 58: (SEQ ID No:138 ; SEQ ID No:139 ; SEQ ID No:140); SET 61:  
(SEQ ID No:147 ; SEQ ID No:148 ; SEQ ID No:149); SET 69: (SEQ ID  
No:168 ; SEQ ID No:169 ; SEQ ID No:170) and SET 182: (SEQ ID  
No:432).

20           7     A polynucleotide library according to Claim  
6 wherein said polynucleotide sequences or subsequences  
thereof of said pool correspond to any combination of at  
least one polynucleotide selected among those included in at  
least 50%, preferably 75% and more preferably 100% of the  
predefined sets.

25           8.    A library according to anyone Claim 1 or 2  
wherein the pool of polynucleotide sequences or subsequences  
correspond substantially to any combination of at least one  
polynucleotide sequence selected among those included in each  
one of predefined polynucleotide sequences sets comprising:

30           SET 11: (SEQ ID No:22 ; SEQ ID No:23 ; SEQ ID No:24)  
; SET 26: (SEQ ID No:59; SEQ ID No:60 ; SEQ ID No:61) ; SET 32:  
(SEQ ID No:76; SEQ ID No:77 ; SEQ ID No:78) ; SET 34: (SEQ ID  
No:82 ; SEQ ID No:83) ; SET 40: (SEQ ID No:97 ; SEQ ID No:98 ; SEQ  
ID No:99) ; SET 57: (SEQ ID No:135 ; SEQ ID No:136 ;SEQ ID No:137)  
; SET 64: (SEQ ID No:156 ; SEQ ID No:157; SEQ ID No:158) ; SET  
35   107: (SEQ ID No:255 ; SEQ ID No:256) ; SET 119: (SEQ ID No:279 ;

SEQ ID No:280 ; SEQ ID No:281) ; SET 136: (SEQ ID No:322 ; SEQ ID No:323) ; SET 140: (SEQ ID No:331 ; SEQ ID No:332 ; SEQ ID No:333) ; SET 141: (SEQ ID No:334; SEQ ID No:335 ; SEQ ID No:336) ; SET 145: (SEQ ID No:345; SEQ ID No:346) ; SET 148: (SEQ ID No:352; SEQ ID No:353) ; SET 149: (SEQ ID No:354 ; SEQ ID No:355) ; SET 162: (SEQ ID No:385; SEQ ID No:386; SEQ ID No:387) ; SET 165: (SEQ ID No:394 ; SEQ ID No:395) ; SET 169: (SEQ ID No:402 ; SEQ ID No:403) ; SET 174: (SEQ ID No:414 ; SEQ ID No:415 ; SEQ ID No:416) and SET 188: (SEQ ID No:442),

wherein said sequences are useful in detecting a hormone sensitive tumor cell

9. A polynucleotide library according to Claim 8 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

10. A library according to Claim 8 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET 136: (SEQ ID No:322 ; SEQ ID No:323) ; SET 145: (SEQ ID No:345 ; SEQ ID No:346); SET 149: (SEQ ID No:354 ; SEQ ID No:355) and SET 169: (SEQ ID No:402 ; SEQ ID No:403)

and of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 11: (SEQ ID No:22 ; SEQ ID No:23 ; SEQ ID No:24) ; SET 40: (SEQ ID No:97 ; SEQ ID No:98 ; SEQ ID No:99); SET 57: (SEQ ID No:135 ; SEQ ID No:136 ; SEQ ID No:137); SET 119: (SEQ ID

No:279; SEQ ID No:280 ; SEQ ID No:281) and SET 174: (SEQ ID No:414 ; SEQ ID No:415 ; SEQ ID No:416)

11. A polynucleotide library according to Claim  
5 10 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

10 12. A library according to anyone Claim 1 or 2 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each  
15 one of predefined polynucleotide sequences sets comprising:

20 SET 8: (SEQ ID No:16) ; SET 11: (SEQ ID No:22 ; SEQ ID No:23 ; SEQ ID No:24) ; SET 18: (SEQ ID No:39 ; SEQ ID No:40 ; SEQ ID No:41) ; SET 25: (SEQ ID No:57 ; SEQ ID No:58) ; SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET 34: (SEQ ID No:82 ; SEQ ID No:83) ; SET 40: (SEQ ID No:97 ; SEQ ID No:98 ; SEQ ID No:99) ; SET 49: (SEQ ID No:118 ; SEQ ID No:119) ; SET 57: (SEQ ID No:135 ; SEQ ID No:136 ; SEQ ID No:137) ; SET 91: (SEQ ID No:216 ; SEQ ID No:217) ; SET 100: (SEQ ID No:238 ; SEQ ID No:239) ; SET 105: (SEQ ID No:250 ; SEQ ID No:251 ; SEQ ID No:252) ; SET  
25 136: (SEQ ID No:322 ; SEQ ID No:323) ; SET 138: (SEQ ID No:326 ; SEQ ID No:327 ; SEQ ID No:328) ; SET 139: (SEQ ID No:329 ; SEQ ID No:330) ; SET 141: (SEQ ID No:334 ; SEQ ID No:335 ; SEQ ID No:336) ; SET 158: (SEQ ID No:374 ; SEQ ID No:375 ; SEQ ID No:376) ; SET 169: (SEQ ID No:402 ; SEQ ID No:403) ; SET 180: (SEQ ID No:430) and SET 186: (SEQ ID No:438 ; SEQ ID No:439),

30 wherein said sequences are useful in differentiating a tumor with lymph nodes from a tumor without lymph nodes.

13. A polynucleotide library according to Claim 12 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

14. A library according to Claim 12 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising

SET 18: (SEQ ID No:39 ; SEQ ID No:40 ; SEQ ID No:41) ; SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET 57: (SEQ ID No:135 ; SEQ ID No:136; SEQ ID No:137); SET 91: (SEQ ID No:216 ; SEQ ID No:217) and SET 105: (SEQ ID No:250 ; SEQ ID No:251 ; SEQ ID No:252)

and of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET 11: (SEQ ID No:22 ; SEQ ID No:23; SEQ ID No:24) ; SET 40: (SEQ ID No:97; SEQ ID No:98 SEQ ID No:99) ; SET 49: (SEQ ID No:118 ; SEQ ID No:119) ; SET 100: (SEQ ID No:238 ; SEQ ID No:239) and SET 141: (SEQ ID No:334; SEQ ID No:335 ; SEQ ID No:336).

15. A polynucleotide library according to Claim 14 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at least 50%, preferably 75% and more preferably 100% of the predefined sets.

16. A library according to anyone of Claims 1 or 2 wherein the pool of polynucleotide sequences or

subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

5                   SET 11: (SEQ ID No:22 ; SEQ ID No:23 ; SEQ ID No:24)  
; SET 22: (SEQ ID No:48 ; SEQ ID No:49 ; SEQ ID No:50) ; SET 23:  
(SEQ ID No:51 ; SEQ ID No:52 ; SEQ ID No:53) ; SET 26: (SEQ ID  
10 No:59 ; SEQ ID No:60 ; SEQ ID No:61) ; SET 28: (SEQ ID No:65 ; SEQ  
ID No:66 ; SEQ ID No:67) ; SET 31: (SEQ ID No:73 ; SEQ ID No:74 ;  
SEQ ID No:75) ; SET 32: (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID  
No:78) ; SET 34: (SEQ ID No:82 ; SEQ ID No:83) ; SET 49: (SEQ ID  
No:118 ; SEQ ID No:119) ; SET 57: (SEQ ID No:135 ; SEQ ID No:136 ;  
SEQ ID No:137) ; SET 64: (SEQ ID No:156 ; SEQ ID No:157 ; SEQ ID  
No:158) ; SET 73: (SEQ ID No:178 ; SEQ ID No:179) ; SET 77: (SEQ ID  
15 No:186) ; SET 81: (SEQ ID No:194 ; SEQ ID No:195) ; SET 95: (SEQ  
ID No:226 ; SEQ ID No:227) ; SET 131: (SEQ ID No:308 ; SEQ ID  
No:309 ; SEQ ID No:310) ; SET 138: (SEQ ID No:326 ; SEQ ID No:327  
; SEQ ID No:328) ; SET 140: (SEQ ID No:331 ; SEQ ID No:332 ; SEQ  
ID No:333) ; SET 149: (SEQ ID No:354 ; SEQ ID No:355) ; SET 162:  
20 (SEQ ID No:385 ; SEQ ID No:386 ; SEQ ID No:387) ; SET 164: (SEQ ID  
No:391 ; SEQ ID No:392 ; SEQ ID No:393) ; SET 165: (SEQ ID No:394  
; SEQ ID No:395) and SET 183: (SEQ ID No:433 ; SEQ ID No:434),

                  wherein said sequences are useful in  
differentiating antracycline-sensitive tumors from  
25 antracycline-insensitive tumors.

17. A polynucleotide library according to Claim  
16 wherein said polynucleotide sequences or subsequences  
thereof of said pool correspond to any combination of at  
30 least one polynucleotide selected among those included in at  
least 50%, preferably 75% and more preferably 100% of the  
predefined sets.

18. A library according to Claim 16 wherein the  
35 pool of polynucleotide sequences or subsequences correspond

substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising

5           SET N° 32: (SEQ ID No:76; SEQ ID No:77; SEQ ID No:78)  
; SET N°136: (SEQ ID No:322 ; SEQ ID No:323) ; SET N° 145: (SEQ ID  
No:345; SEQ ID No:346) ; SET N° 149: SEQ ID No:354; SEQ ID No:355)  
; SET N°169: (SEQ ID No:402 ; SEQ ID No:403)

10           and of at least one polynucleotide sequence  
selected among those included in each one of predefined  
polynucleotide sequences sets comprising:

15           SET No 11: (SEQ ID No:22; SEQ ID No:23 ; SEQ ID  
No:24); SET No 40: (SEQ ID No:97 ; SEQ ID No:98 ; SEQ ID No:99) ;  
SET No 57: (SEQ ID No:135 ; SEQ ID No:136 ; SEQ ID No:137) ; SET  
No 119: (SEQ ID No:279 ; SEQ ID No:280 ; SEQ ID No:281) ; SET No  
174: (SEQ ID No:414 ; SEQ ID No:415; SEQ ID No:416).

20           19. A polynucleotide library according to Claim  
18 wherein said polynucleotide sequences or subsequences  
thereof of said pool correspond to any combination of at  
least one polynucleotide selected among those included in at  
least 50%, preferably 75% and more preferably 100% of the  
predefined sets.

25           20. A library according to anyone of Claims 1 or  
2 wherein the pool of polynucleotide sequences or  
subsequences correspond substantially to any combination of  
at least one polynucleotide sequence selected among those  
included in each one of predefined polynucleotide sequences  
sets comprising

30           SET No 14 (SEQ ID No:30; SEQ ID No:31) ; SET No 23  
(SEQ ID No:51; SEQ ID No:52; SEQ ID No:53) ; SET No 25 (SEQ ID  
No:57; SEQ ID No:58) ; SET No 27 (SEQ ID No:62; SEQ ID No:63; SEQ  
ID No:64) ; SET No 28 (SEQ ID No:65; SEQ ID No:66; SEQ ID No:67) ;  
SET No 32 (SEQ ID No:76; SEQ ID No:77; SEQ ID No:78) ; SET No 39  
35           (SEQ ID No:94; SEQ ID No:95; SEQ ID No:96) ; SET No 41 (SEQ ID

No:100; SEQ ID No:101; SEQ ID No:78) ; SET No 44 (SEQ ID No:106; SEQ ID No:107; SEQ ID No:108) ; SET No 48 (SEQ ID No:115; SEQ ID No:116; SEQ ID No:117) ; SET No 51 (SEQ ID No:122; SEQ ID No:78) ; SET No 64 (SEQ ID No:156; SEQ ID No:157; SEQ ID No:158) ; SET No 81 (SEQ ID No:194; SEQ ID No:195) ; SET No 83 (SEQ ID No:199; SEQ ID No:200) ; SET No 91 (SEQ ID No:216; SEQ ID No:217) ; SET No 96 (SEQ ID No:228; SEQ ID No:229) ; SET No 99 (SEQ ID No:235; SEQ ID No:236; SEQ ID No:237) ; SET No 108 (SEQ ID No:257; SEQ ID No:258) ; SET No 110 (SEQ ID No:262; SEQ ID No:200) ; SET No 116 (SEQ ID No:273; SEQ ID No:274) ; SET No 117 (SEQ ID No:275; SEQ ID No:276) ; SET No 118 (SEQ ID No:277; SEQ ID No:278) ; SET No 120 (SEQ ID No:282; SEQ ID No:283; SEQ ID No:276) ; SET No 126 (SEQ ID No:296; SEQ ID No:297;) ; SET No 142 (SEQ ID No:337; SEQ ID No:338; SEQ ID No:117) ; SET No 144 (SEQ ID No:342; SEQ ID No:343; SEQ ID No:344) ; SET No 149 (SEQ ID No:354; SEQ ID No:355) ; SET No 152 (SEQ ID No:361; SEQ ID No:31) ; SET No 153 (SEQ ID No:362; SEQ ID No:363; SEQ ID No:364) ; SET No 154 (SEQ ID No:365; SEQ ID No:366; SEQ ID No:367) ; SET No 157 (SEQ ID No:372; SEQ ID No:373; SEQ ID No:108) ; SET No 159 (SEQ ID No:377; SEQ ID No:378; SEQ ID No:379) ; SET No 162 (SEQ ID No:385; SEQ ID No:386; SEQ ID No:387) ; SET No 166 (SEQ ID No:396; SEQ ID No:397; SEQ ID No:398) ; SET No 167 (SEQ ID No:399; SEQ ID No:400; SEQ ID No:117) ; SET No 168 (SEQ ID No:401) ; SET No 171 (SEQ ID No:406; SEQ ID No:407; SEQ ID No:408) ; SET No 172 (SEQ ID No:409; SEQ ID No:410; SEQ ID No:411) ; SET No 173 (SEQ ID No:412; SEQ ID No:413) ; SET No 176 (SEQ ID No:420; SEQ ID No:421; SEQ ID No:422) ; SET No 177 (SEQ ID No:423; SEQ ID No:424; SEQ ID No:425) ; SET No 178 (SEQ ID No:426; SEQ ID No:427; SEQ ID No:428) ; SET No 179 (SEQ ID No:429; SEQ ID No:408) ; SET No 184 (SEQ ID No:435; SEQ ID No:436) ; SET No 185 (SEQ ID No:437),

wherein said sequences are useful in classifying good and poor prognosis primary breast tumors.

21. A polynucleotide library according to Claim 20 wherein said polynucleotide sequences or subsequences thereof of said pool correspond to any combination of at least one polynucleotide selected among those included in at

least 50%, preferably 75% and more preferably 100% of the predefined sets.

22. A library according to Claim 20 wherein the pool of polynucleotide sequences or subsequences correspond substantially to any combination of at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising

SET N° 23 (SEQ ID No:51 ; SEQ ID No:52 ; SEQ ID No:53) ; SET N° 25 (SEQ ID No:57 ; SEQ ID No:58) ; SET N° 32 (SEQ ID No:76 ; SEQ ID No:77 ; SEQ ID No:78) ; SET N° 41 (SEQ ID No:100 ; SEQ ID No:101 ; SEQ ID No:78) ; SET N° 48 (SEQ ID No:115 ; SEQ ID No:116 ; SEQ ID No:117) ; SET N° 51 (SEQ ID No:122 ; SEQ ID No:78) ; SET N° 64 (SEQ ID No:156 ; SEQ ID No:157 ; SEQ ID No:158) ; SET N° 81 (SEQ ID No:194 ; SEQ ID No:195) ; SET N° 83 (SEQ ID No:199 ; SEQ ID No:200) ; SET N° 91 (SEQ ID No:216 ; SEQ ID No:217) ; SET N° 99 (SEQ ID No:235 ; SEQ ID No:236 ; SEQ ID No:237) ; SET N° 110 (SEQ ID No:262 ; SEQ ID No:200) ; SET N° 116 (SEQ ID No:273 ; SEQ ID No:274) ; SET N° 142 (SEQ ID No:337 ; SEQ ID No:338 ; SEQ ID No:117) ; SET N° 144 (SEQ ID No:342 ; SEQ ID No:343 ; SEQ ID No:344) ; SET N° 149 (SEQ ID No:354 ; SEQ ID No:355) ; SET N° 162 (SEQ ID No:385 ; SEQ ID No:386 ; SEQ ID No:387) ; SET N° 167 (SEQ ID No:399 ; SEQ ID No:400 ; SEQ ID No:117) ; SET N° 171 (SEQ ID No:406 ; SEQ ID No:407 ; SEQ ID No:408) ; SET N° 172 (SEQ ID No:409 ; SEQ ID No:410 ; SEQ ID No:411) ; SET N° 173 (SEQ ID No:412 ; SEQ ID No:413) ; SET N° 176 (SEQ ID No:420 ; SEQ ID No:421 ; SEQ ID No:422) ; SET N° 177 (SEQ ID No:423 ; SEQ ID No:424 ; SEQ ID No:425) ; SET N° 178 (SEQ ID No:426 ; SEQ ID No:427 ; SEQ ID No:428) ; SET N° 179 (SEQ ID No:429 ; SEQ ID No:408) ; SET N° 184 (SEQ ID No:435 ; SEQ ID No:436) ; SET N° 185 (SEQ ID No:437),

and at least one polynucleotide sequence selected among those included in each one of predefined polynucleotide sequences sets comprising:

SET No 14 (SEQ ID No:30 ; SEQ ID No:31) ; SET No 27 (SEQ ID No:62 ; SEQ ID No:63 ; SEQ ID No:64) ; SET No 28 (SEQ ID



No:65 ; SEQ ID No:66 ; SEQ ID No:67) ; SET No 39 (SEQ ID No:94 ;  
SEQ ID No:95 ; SEQ ID No:96) ; SET No 44 (SEQ ID No:106 ; SEQ ID  
No:107 ; SEQ ID No:108) ; SET No 96 (SEQ ID No:228 ; SEQ ID  
No:229) ; SET No 108 (SEQ ID No:257 ; SEQ ID No:258) ; SET No 117  
5 (SEQ ID No:275 ; SEQ ID No:276) ; SET No 118 (SEQ ID No:277 ; SEQ  
ID No:278) ; SET No 120 (SEQ ID No:282 ; SEQ ID No:283 ; SEQ ID  
No:276) ; SET No 126 (SEQ ID No:296 ; SEQ ID No:297) ; SET No 152  
(SEQ ID No:361 ; SEQ ID No:31) ; SET No 153 (SEQ ID No:362 ; SEQ  
ID No:363 ; SEQ ID No:364) ; SET No 154 (SEQ ID No:365 ; SEQ ID  
10 No:366 ; SEQ ID No:367) ; SET No 157 (SEQ ID No:372 ; SEQ ID  
No:373 ; SEQ ID No:108) ; SET No 159 (SEQ ID No:377 ; SEQ ID  
No:378 ; SEQ ID No:379) ; SET No 166 (SEQ ID No:396 ; SEQ ID  
No:397 ; SEQ ID No:398) ; SET No 168 (SEQ ID No:401),

wherein the combination of overexpression of the  
15 genes identified by said first group of cluster sequences  
with the underexpression of the genes identified by said  
second group of cluster sequences are useful in classifying  
good and poor prognosis primary breast tumors.

20 23. A polynucleotide library according to Claim  
22 wherein said polynucleotide sequences or subsequences  
thereof of said pool correspond to any combination of at  
least one polynucleotide selected among those included in at  
least 50%, preferably 75% and more preferably 100% of the  
25 predefined sets.

24. A polynucleotide library according to anyone  
of Claims 1 to 23 wherein said tumor cells are breast tumor  
cells.

30 25. A polynucleotide library according to any of  
Claims 1 to 23 wherein said polynucleotides are immobilized  
on a solid support in order to form a polynucleotide array.

26. A polynucleotide library according to Claim 25 wherein the support is selected from the group comprising a nylon membrane, nitrocellulose membrane, glass slide, glass beads, membranes on glass support or a silicon chip.

5

27. A polynucleotide array useful for prognosis or diagnostic of tumor comprising an immobilized polynucleotide library according to Claims 1 to 3.

10

28. A polynucleotide array useful to differentiate a normal cell from a cancer cell comprising any combination of immobilized polynucleotide sequences sets according to claims 4 to 7.

15

29. A polynucleotide array useful to detect a hormone sensitive tumor cell comprising any combination of immobilized polynucleotide sequences sets according to claims 8 to 11.

20

30. A polynucleotide array useful to differentiate a tumor with lymph nodes from a tumor without lymph nodes comprising any combination of immobilized polynucleotide sequences sets according to claims 12 to 15.

25

31. A polynucleotide array useful to differentiate antracycline-sensitive tumors from antracycline-insensitive tumors comprising any combination of immobilized polynucleotide sequences sets according to claims 16 to 19.

30

32. A polynucleotide array useful to classify good and poor prognosis primary breast tumors comprising any

combination of immobilized polynucleotide sequences sets according to claim 20 to 23.

5 33. A method of detecting differentially expressed polynucleotide sequences which are correlated with a cancer, said method comprising:

a) obtaining a polynucleotide sample from a patient and

10 b) reacting said polynucleotide sample obtained in step (a) with a probe immobilized on a solid support wherein said probe comprises any combination of the polynucleotide sequences of the polynucleotide library of Claims 1 to 23 or any combination of expression products encoded by any of the polynucleotide sequences of the  
15 libraries of Claims 1 to 23 and

c) detecting the reaction product of step (b).

20 34. A method for detecting differentially expressed polynucleotide sequences according to Claim 33 wherein said polynucleotide sample is labeled before its reaction step.

25 35. A method for detecting differentially expressed polynucleotide sequences according to Claim 34 wherein the label of the polynucleotide sample is selected from the group consisting of radioactive, colorimetric, enzymatic, molecular amplification, bioluminescent or fluorescent labels.

30 36. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 35 further comprising obtaining a control polynucleotide sample, reacting said control sample with said probe

detecting a control sample reaction product and comparing the amount of said polynucleotide sample reaction product to the amount of said control sample reaction product.

5                   37. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 36 wherein the polynucleotide sample is cDNA, RNA or mRNA.

10                   38. A method for detecting differentially expressed polynucleotide sequences according to Claim 37 wherein mRNA is isolated from said polynucleotide sample and cDNA is obtained by reverse transcription of said mRNA.

15                   39. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 38 wherein said reaction step is performed by hybridising the polynucleotide sample with the probe.

20                   40. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 39 wherein said method is used for detecting, diagnosing, staging, monitoring, predicting, preventing or treating conditions associated with cancer.

25                   41. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 40 wherein the cancer is breast cancer.

30                   42. A method for detecting differentially expressed polynucleotide sequences according to Claims 33 to 41 wherein the product encoded by any of the polynucleotide sequences or polynucleotide sequences sets is involved in a receptor-ligand reaction on which detection is based.

43. A method for screening an anti-tumor agent comprising the method of Claim 33 wherein said polynucleotide sample is obtained from a patient treated with the anti-tumor agent to be screened.

Figure 1

Figure 1A Normal Breast

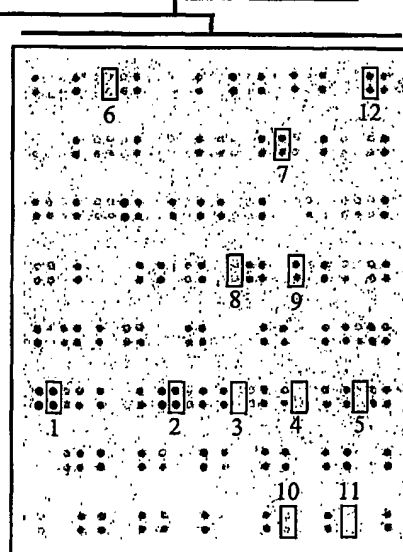
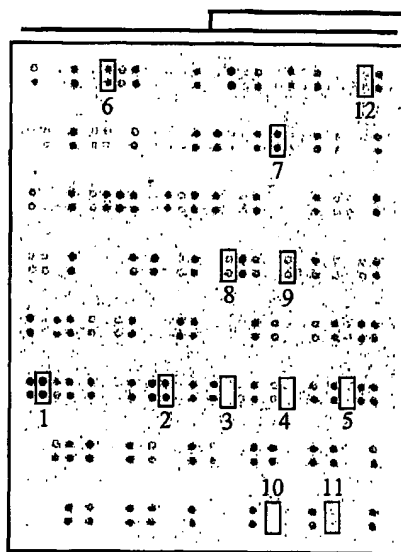
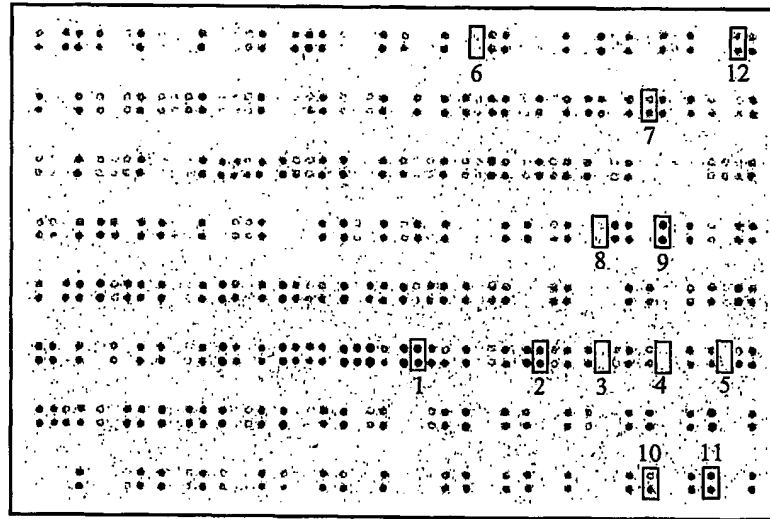


Figure 1B

ER-

ER+

Figure 1C

Breast cancer

Figure 2

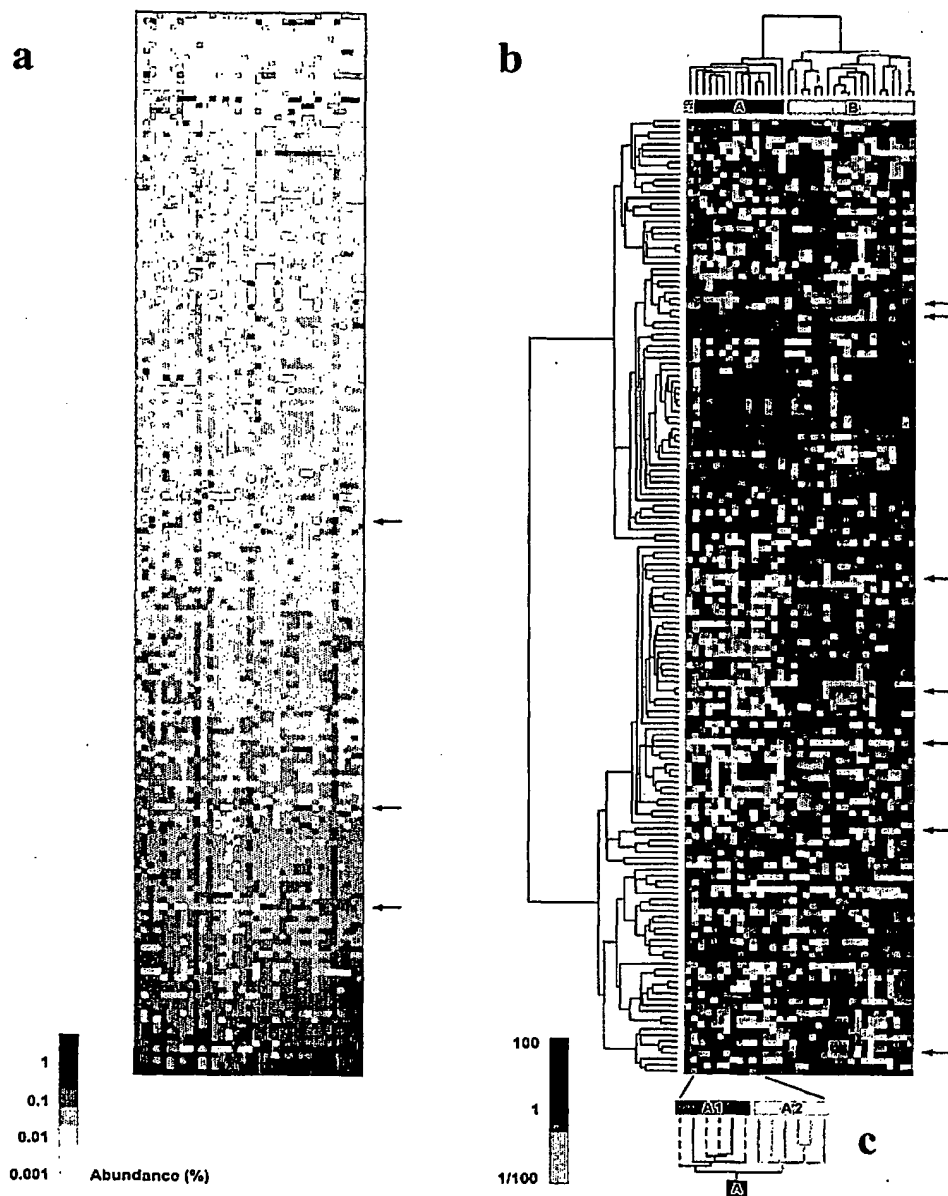


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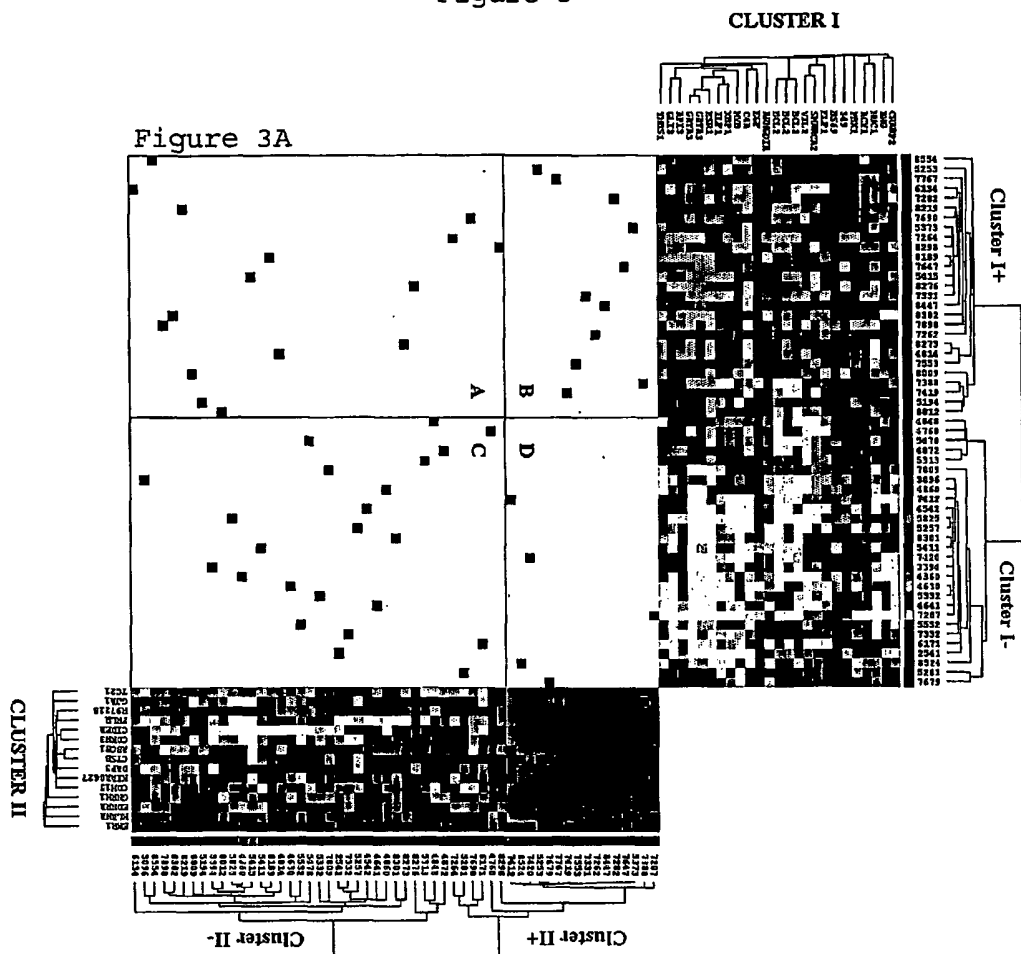


Figure 3C

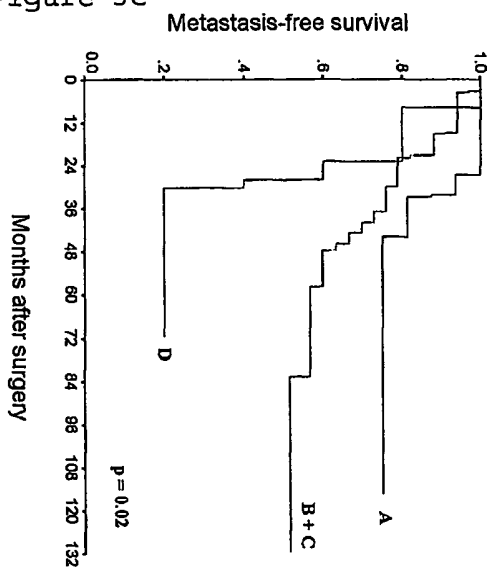


Figure 3B

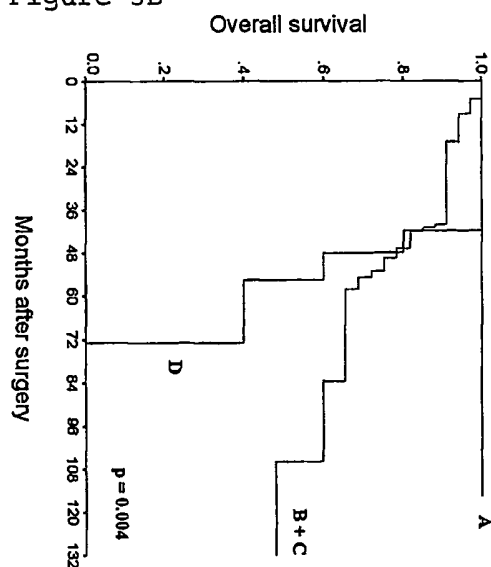




Figure 4

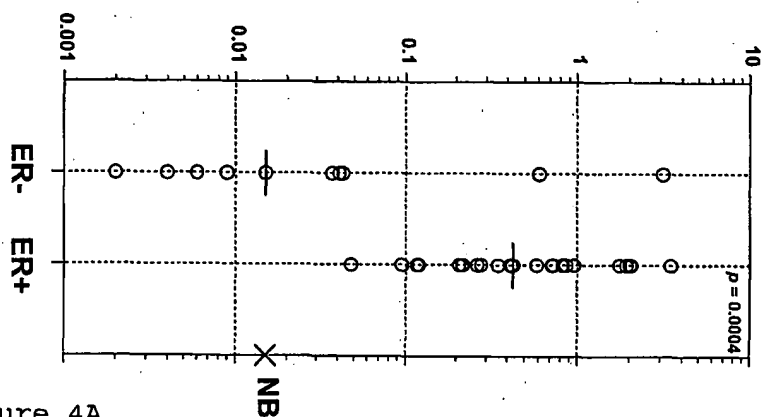


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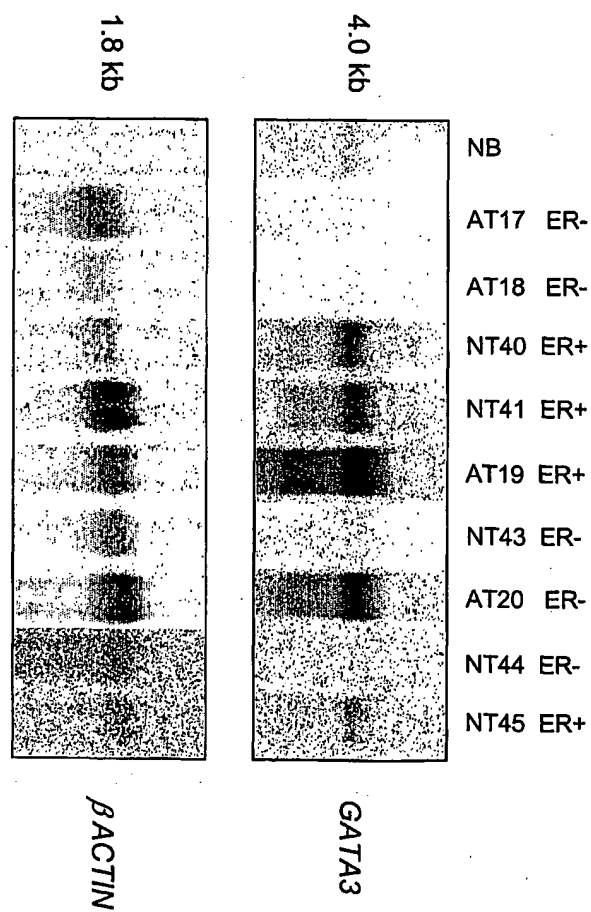


Figure 4B

## SEQUENCE LISTING

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<110> François Bertucci  
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<120> cDNA arrays and their use for gene  
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&lt;223&gt; hiv-1 rev binding protein (HRB) gene.

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<222> (1)..(417)

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tgaccccta ctgggctcac ccacgggctc cttcccaca ggcccatgc ccccaccac 1320
cagcactact gtggtggctc cgctcagctc atgagggcac agagcatggc ctccagagga 1380
ggggtgtgt ctttctctc ttgtagccag aattctggac aaccaagtc tctgggccc 144 0
aggcaccccc tggcttgaac cttcaaagct tttgtaaaat aaaaccacca aagtcctg 1498
```

<210> 5

<211> 423  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(423)  
<223> 5' terminal sequence. t tousled-like kinase 2  
(TLK2) gene.

<400> 5  
ggcacgagga gaatacgatt cttaaagcta ctgaagtgca gttcccgcga aagccagtag 60  
taacacctga agcaaaggcg tttattcgac gatgcttggc ctaccgaaag aggaccgcat 120  
tgatgtccag cagctggcct gtgatcccta cttgttgctt cacatccgaa agtcagtctc 180  
tacaagtagc cctgctggag ctgctattgc atcaacctct ggggcgtcca ataacagttc 240  
ttctaattga gactgactcc aaggccacaa actgttcaac acacacaaag tgggacaaat 300  
gggcgtttca gcaggcgggt ttgggaacat aggcgaatcc gaatgggtac ttgatggaaa 360  
cctgttacca ggtgnttttt attttatttg aattttttt t nccatncctt agaggcttgg 420  
aca 423

<210> 6  
<211> 3327  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(3327)  
<223> tousled-like kinase 2 (TLK2) gene.

<400> 6  
ccgggcgggg ggttgcggcg ctcaggagag gccccggctc cgccccgggc ctgccaggg 60  
ggagagcgga gctccgcagc cgggtcgggt cggggcccct cccgggagga gcgtggagcg 120  
cggcggcgcg ggccgcagca gaaatgatgg aagaattgca tagcctggac ccacgacgg c 180  
aggaattatt ggaggccagg tttactggag taggtgttag taagggacca cttaatagtg 240  
agtcttccaa ccagagcttg tgcagcgtcg gataccttag tgataaagaa gtagagactc 300  
ccgagaaaaa gcagaatgac cagcgaaatc ggaaaagaaa agctgaacca tatgaaacta 360  
gccaaaggga aggcactcct aggggacata aaattag tga ttactttgag tttgctgggg 420  
gaagcgcgcc aggaaccagc cctggcagaa gtgttccacc agttgcacga tcctcaccgc 480  
aacattcctt atccaatccc ttaccgcgac gactagaaca gcccctctat ggttttagatg 540  
gcagtgtctg aaaggaggca acggaggagc agtctgctct gccaacctc atgtcagtga 600  
tgctagcaaa acctcggctt gacacagagc agctggcgca aaggggagct ggctctgct 660  
tcacttttgt ttcagctcag caaaacagtc cctcatctac gggatctggc aacacagagc 720  
attcctgcag ctcccaaaaa cagatctcca tccagcacag acggaccag tccgacctca 780  
caatagaaaa aatatctgca ctagaaaaca gtaagaattc tgacttagag aagaagg agg 840  
gaagaataga tgatttatta agagccaact gtgatttgag acggcagatt gatgaacagc 900  
aaaagatgct agagaaatac aaggaacgat taaatagatg tgtgacaatg agcaagaaac 960  
tccttagata aaagtcaaaa caagagaaga tggcgtgtag agataagagc atgcaagacc 1020  
gcttgagact gggccaacttt actactgtcc gaca cggagc ctcatttact gaacagtga 1080  
cagatggtta tgcttttcag aatcttatca agcaacagga aaggataaat tcacagaggg 1140  
aagagataga aagacaacgg aaaaatgttag caaagcggaa acctcctgcc atgggtcagg 1200  
cccctctgac aaccaatgag cagaaacagc ggaaaagcaa gaccaatgga gctgaaaatg 1260  
aaacgttaac gttagcagaa taccatgaac aagaagaaat cttcaaactc agattaggtc 1320  
atcttaaaaa ggaggaagca gagatccagg cagagctgga gagactagaa agggtagaa 1380

5/292

```
atctacatat cagggaaacta aaaaggatac ataatgaaga taattcacaa tttaaagatc 1440
atccaacgct aaatgacaga tatttggttgt tacatctttt gggtagag ga ggtttcagt 1500
aagttttacaa ggcatgtgat ctaacagagc aaagatacgt agctgtgaaa attcaccagt 1560
taaataaaaa ctggagagat gagaaaaagg agaattacca caagcatgca tgtagggaat 1620
accggattca taaagagctg gatcatcca gaatagttaa gctgtatgat tacttttcac 1680
tggatactga ctgtttttgt ac agtattag aatactgtga gggaaatgat ctggacttct 1740
acctgaaaca gcacaaatta atgtcggaga aagaggcccg gtccattatc atgcagattg 1800
tgaatgcttt aaagtactta aatgaaataa aacctcccat catacactat gacctcaaac 1860
caggtaatat tcttttagta aatggtacag cgtgtggaga gataaaaatt acagattttg 1 920
gtctttcgaa gatcatggat gatgatagct acaattcagt ggatggcatg gagctaact 1980
cacaagggtgc tggacttat tggatattac caccagagtg ttttgtggtt gggaaagaac 2040
caccaaagat ctcaataaaa gttgatgtgt ggtcgggtgg tgtgatcttc tatcagtgtc 2100
tttatggaag gaagcctttt gccataaacc agtctc agca agacatccta caagagaata 2160
cgattcttaa agctactgaa gtgcagttcc cgccaaagcc agtagtaaca cctgaagcaa 2220
aggcgtttat tcgaacgatgc ttggcctacc gaaagaggga ccgcattgat gtccagcagc 2280
tggcctgtga tccctacttg ttgcctcaca tccgaaagtc agtctctaca agtagccctg 2340
ctggagctgc tattgcatca acctctgggg cgtccaataa cagttcttct aattgagact 2400
gactccaagg ccacaaactg ttcaacacac acaaagtggg caaatggcgt tcagcagcgg 2460
gtttggaaca tagcgaatcc gaatggatct gatgaaacct gtaccaggtg cttttatttt 2520
cttgcttttt tcccatccat agagcatgac agcatcgatt ctcataggag agaaaccttg 2580
ggcagctccg gccaggcctt gtaggaaaag gccccgcccc aggttccagc gtcaacggcc 2640
actgtgtgtg gctgctctga gtgaggaaaa aattaaaaag aaaaactggt tccatgtact 2700
gtgaacttga aaacttgcag actcaggggg gtccctgatg cagtgcctca gatgaagaat 2760
gtggacttga aaatacacagac tggg ctatgc cagtgtctat atttaaactt gttcttttct 2820
tttaataaag tttaggtaac atctcctgaa aagctttagt cacaaaggct cagctgggga 2880
tgggtgttga cttcggagga aaaaagttgc tattgcccgt taaaggcact agagttagtg 2940
ttttatccct aaataatttc aatttttaaa aacatgcagc ttccctctcc ccttttttat 300 0
ttttgaaaga atacatttgg tcataaagtg aaaccgctat tagcaagtac gaggcaatgt 3060
tcattccaat cagatgcagc ttctcctcc gtctggtctc ctgtttgcaa ttgcttccct 3120
catctcagta gggaaaaaat tgagtgggag tactgagatg tgtgggtttt tgccattgga 3180
caaagaatga ggtagaaga ctgcagcttg gagtctct ct aggttttcaa ctatttcttc 3240
acaatttgaa cacttgacgg ttgtcccttt taattttatt gaagtgtat ttttttaaat 3300
aaaggttcat ctgtccatgc aaaaaaa 3327
```

&lt;210&gt; 7

&lt;211&gt; 300

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(300)

<223> 3' terminal sequence. ests, weakly similar  
to alu7\_human alu subfamily sq sequence  
contamination warning entry [h.sapiens] (EST  
T81919) gene.

&lt;400&gt; 7

```
tncaagagac aggggttnngc acattgccca ggatggtctc aaactcctag agttgagcta 60
tccacccacc tttggcctnc caaagtgtctg ggatcacagg cgtgagtcac tgnntccagc 120
acccatctgg aggtcttctta aagcccaggc cccacgccga gcttctgagt caataaagaa 180
gtctgcattt ctaacaagct tctaggggat gctgctgctg ctgctggtcc aggggccccca 240
ctttgaagaa ccactgcact gggtntttcc tctgggaccc gaatgcctgt gcttctcccc 300
```

&lt;210&gt; 8

&lt;211&gt; 369

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(369)

<223> 5' terminal sequence. ests, weakly similar  
to alu7\_human alu subfamily sq sequence  
contamination warning entry [h.sapiens] (EST  
T81919) gene.

<400> 8

```
cctaacgcag gtttccccgc aaatgactgg tcacgcggga ctgaacaccg cacaggcagg 60
aggcatggca agggtaagtg aa ctgaagca ctttcaatac ttctaccta accgcgggct 120
ttccctccga gtaatgcgta aaatgggacc acgtggccca ctctgtttt tctctttggg 180
ctctccacgt gccactcatg cttggaagag acagatttct ttctaggata aagatctctg 240
ccccatttct gtcttttaaa atggagaatt ctttaaagaa gtagggacag cttncagggt 300
cagggcagtt tgggaaagtn acaggggcct aattgtgttc cgtggaaacn ggggtaggag 360
gtttgcttt                                     369
```

<210> 9

<211> 255

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(255)

<223> 3' terminal sequence. cyclin d1 (prad1:  
parathyroid adenomatosis 1) (CCND1) gene.

<400> 9

```
aaagacagtt tttgggtaat cttttncttt tgcttaagtc agagatggaa gggggaaaga 60
gcaaaggaaa aaacaaccaa caacaaggag aatgaagctt tcccttctgg tatcaaaatg 120
ctccggagag gagggactnt cagtggagca cctggggccg gctccgcctc gctgcgggtg 180
gcggtggcgc cctngcctg ggccttcag atgtccacgt cccgcacgtc ggtgggtntg 240
caagccaggt ccacc                                     255
```

<210> 10

<211> 1325

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(1325)

<223> cyclin d1 (prad1: parathyroid adenomatosis  
1) (CCND1) gene.

<400> 10

```
gcagtagcag cgagcagcag agtccgcac g ctccggcgag gggcagaaga gcgcgagggga 60
gcgcgggggca gcagaagcga gagccgagcg cggaccacag caggaccac agccctccc 120
agctgcccag gaagagcccc agccatggaa caccagctcc tgtgctgca agtgaaacc 180
atccgcccgc cgtaccccga tgccaacctc ctcaacgacc ggggtgctgcg ggccatgctg 240
aaggcggagg agacctgccc gccctcggtg tcctacttca aatgtgtgca gaaggaggtc 300
ctgccgtcca tgcggaagat cgtcgccacc tggatgctgg aggtctgca ggaacagaag 360
tgcgaggagg aggtcttccc gctggccatg aactacctgg accgcttcct gtcgctggag 420
cccgtgaaaa agagccgctt gcagctgctg ggggccactt gcatgttcgt ggcctctaag 480
atgaaggaga ccatccccct gacggccgag aagctgtgca tctacaccga cggctccatc 540
cggcccgagg agctgctgca aatggagctg ctctggtga acaagctcaa gtggaacctg 600
gccgcaatga cccgcacga ttcatgtga cacttcctct ccaaaatgcc agaggcggag 660
gagaacaaac agatcatccg caaacacg cg cagaccttcg ttgcctcttg tgccacagat 720
gtgacgttca ttccaatcc gccctccatg cggcagcgg ggagcgtggt ggccgcagtg 780
caaggcctga acctgaggag cccaacaac ttctgtcct actaccgct caccgcttc 840
ctctccagag tgatcaagtg tgaccagac tgctccggg cctgccagga gcagatcgaa 900
gccctgctgg agtcaagcct gcgccaggcc cagcagaaca tggaccccaa ggccgccgag 960
gaggaggaag aggaggagga ggaggtggac ctggttgca caccaccga cgtgcgggac 1020
gtggacatct gaggggcccc ggaggcggg cgccaccgcc accgcagcg agggcggagc 1080
cggccccagg tgctccacat gacagtccct cctctccgga gcattt tgat accagaaggg 1140
aaagcttcat ttctcttgtt ttggttgggt ttctcttgg ctctttccc cttccatctc 1200
tgacttaagc aaaaagaaaa gattacccaa aaactgtctt taaaagagag agagagaaaa 1260
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1320
aaaaa 1325
```

<210> 11  
<211> 449  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(449)  
<223> 5' terminal sequence. signal transducer and  
activator of transcription 1, 91kd (STAT1) gene.

```
<400> 11
atttgaagt caaagtotta ttgataaag atgtgaatga gagaaatata gtaaaaggat 60
ttaggaagtt caacattttg ggcacgcaca caaaagtgat gaacatggag gagtccacca 120
atggcagctt ggcggtgaa ttccggcacc tgcaattgaa agaacaga aa aatgctggca 180
ccagaacgaa tgagggtcct ctcatcgta ctgaagagct tcactccctt agttttgaaa 240
ccaattgtg ccagcctggg ttggtaatt gacctcgaga cgacctctt gcccgttgtg 300
ggtgatctcc aacgtcagcc agctcccag cgggtggggc ctccattcct ttgggtacaa 360
catgctgggt ngcggggaac ccgggg antc tgttccttnt ttcttgact ccaccatgtg 420
ncacggtggg gtttcagntt ttcagaagt 449
```

<210> 12  
<211> 4003  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(4003)



<223> signal transducer and activator of  
transcription 1, 91kd (STAT1) gene.

<400> 12

```
attaaacctc tcgccgagcc cctccgcaga ctctgcgcgc gaaagtttca tttgctgtat 60
gccatcctcg agagctgtct aggttaacgt tcgcactctg tgtatataac ctogacagtc 120
ttggcaccta acgtgctgtg cgtagctgct cctttgggtg aatccccagg cccttggttg 180
ggcacaaggt ggcagatgt ctcagtggta cgaacttcag cagcttgact caaaattcct 240
ggagcaggtt caccagcttt atgatgacag ttttcccatg gaaatcagac agtacctggc 300
acagtgttta gaaaagcaag actgggagca cgctgccaat gatgttt cat ttgccaccat 360
ccgttttcat gacctcctgt cacagctgga tgatcaatat agtcgctttt ctttgagaa 420
taacttcttg ctacagcata acataaggaa aagcaagcgt aatcttcagg ataattttca 480
ggaagacca atccagatgt ctatgatcat ttacagctgt ctgaaggaa aaaggaaaat 540
totgaaaac gccagagat ttaat caggc tcagtcgggg aatattcaga gcacagtgtat 600
gttagacaaa cagaaagagc ttgacagtaa agtcagaaat gtgaaggaca aggttatgtg 660
tatagagcat gaaatcaaga gcctggaaga tttacaagat gaatatgact tcaaatacaa 720
aaccttgtag aacagagaac acgagacca tggtgtggca aagagtgatc agaaacaaga 780
acagctgtta ctcaagaaga tgtatttaat gcttgacaat aagagaaagg aagtagttca 840
caaaataata gagttgctga atgtcactga acttaccag aatgccctga ttaatgatga 900
actagtggag tggaagcgga gacagcagag gcctgtatt gggggggcgc ccaatgcttg 960
cttggtacag ctgcagaact gggtcactat agttgcggag agtct gcagc aagttcggca 1020
gcagcttaaa aagttggagg aattggaaca gaaatacacc tacgaacatg accctatcac 1080
aaaaaaciaa caagtgttat gggaccgcac cttcagtctt ttccagcagc tcattcagag 1140
ctcgtttgtg gtggaagac agcctgcat gccaacgcac cctcagaggc cgctggctct 1200
gaagacaggg gtccagttca ctgtgaagtt gagactgttg gtgaaattgc aagagctgaa 1260
ttataatttg aaagtcaaag tcttatttga taaagatgtg aatgagagaa atacagtaaa 1320
aggatttagg aagttcaaca ttttgggcac gcacacaaaa gtgatgaaca tggaggagtc 1380
caccaatggc agtctggcgg ctgaatttgc gcacctgcaa ttgaaagaac agaaaaatg c 1440
tgccaccaga acgaatgagg gtctctcat cgttactgaa gagcttact cccttagttt 1500
tgaaaccaa ttgtgccagc ctggttttgt aattgacctc gagacgacct ctctgccctg 1560
tgtgtgtatc tccaacgtca gccagctccc gagcgggttg gcctccatcc tttggtacaa 1620
catgctggtg gcggaaccca ggaatctgtc ctt cttcctg actccacat gtgcacgatg 1680
ggctcagctt tcagaagtgc tgagttggca gttttcttct gtcacaaaaa gaggtctcaa 1740
tgtggaccag ctgaacatgt tgggagagaa gctcttgggt cctaacgcca gccccgatgg 1800
tctcattccg tggacgaggt tttgtaagga aaatataaat gataaaaaat ttcccttctg 1860
gctttggatt gaaagcatcc tagaactcat taaaaaacac ctgctccctc tctggaatga 1920
tggtgtcatc atgggcttca tcagcaagga gcgagagcgt gccctgttga aggaccagca 1980
gccggggacc ttctgtctgc ggttcagtga gagctcccgg gaaggggcca tcacattcac 2040
atgggtggag cgggtcccaga acggaggcga acctgacttc catgagg ttg aaccctacac 2100
gaagaagaaa ctttctgtct ttactttccc tgacatcatt cgcaattaca aagtcattggc 2160
tgctgagaa atctctgaga atcccctgaa gtatctgtat ccaaattatg acaaagacca 2220
tgcccttggg aagtattact ccaggccaaa ggaagcacca gagccaatgg aacttgatgg 2280
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tagacttcag accacagaca acctgctccc catgtctcct gaggagtgtg acgaggtgtc 2400
tcggatagtg ggctctgtag aattcgacag tatgatgaac acagtataga gcatgaattt 2460
ttttcatctt ctctggcgag agttttcctt ctcatctgtg attccctcct gctactctgt 2520
tcttcaaat cctgtgtttc tagggaaatg aaagaaaggc cagcaaattc gctgcaacct 2580
gttgatagca agtgaatttt tctctaactc agaaacatca gttactctga agggcatcat 2640
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aacatccaga tacaccocaa gtatcaggac gagaa tgagg gtcctttggg aaaggagaag 2760
ttaagcaaca tctagcaaat gttatgcata aagtcagtgc ccaactgtta taggttgttg 2820
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aattcttaca tgttttcttt gctttaagtg taactggcag ttttccattg gtttacctgt 2940
gaaatagttc aaagccaaat ttatatcaa ttatatcagt cctctttcaa aggtagccat 3000
catggtactg gtgaggggaa aatgtgtatt ttattacatc ttccacattg gctattttaa 3060
gacaaagaca aattctgttt cttgagaaga gaatattagc ttactgttt gttatggctt 3120
aatgacacta gctaatatca atagaaggat gtacatttcc aaattcaca a gttgtgtttg 3180
atatccaaag ctgaatacat tctgctttca tctgtgtcac atacaattat ttttacagtt 3240
ctcccaaggg agttaggcta ttcacaacca ctattcaaaa agttgaaatt aaccatagat 3300
gtagataaac tcagaaattt aattcatgtt tcttaaatgg gctactttgt cctttttgtt 3360
attaggtgtg tatttagtct att agccaca aaattgggaa aggagtagaa aaagcagtaa 3420
```

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ctgacaactt gaataatata ccagagataa tatgagaatc agatcatttc aaaactcatt 3480
tcctatgtaa ctgcattgag aactgcataat gtttcgctga tatatgtgtt tttcacattt 3540
gcgaatgggt ccattctctc tcctgtactt tttccagaca cttttttgag tggatgatgt 36 00
ttcgtgaagt atactgtatt ttaccttttt tccttcctta tcaactgacac aaaaagtaga 3660
ttaagagatg ggtttgacaa ggttcttccc ttttacatac tgctgtctat gtggctgtat 3720
cttgtttttc cactactgct accacaacta tattatcatg caaatgctgt attcttcttt 3780
ggtggagata aagattttctt gagttttgtt ttaaaat taa agctaaagta tctgtattgc 3840
attaaatata atatcgacac agtgctttcc gtggcactgc atacaatctg aggcctcttc 3900
tctcagtttt tatatagatg gcgagaacct aagtttcagt tgattttaca attgaaatga 3960
ctaaaaaaca aagaagacaa cattaaaaac aatattgttt cta 4003

```

&lt;210&gt; 13

&lt;211&gt; 167

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(167)

&lt;223&gt; 3' terminal sequence. fibroblast growth

factor receptor 2 (bacteria -expressed kinase,  
keratinocyte growth factor receptor, craniofacial  
dysostosis 1, crouzon syndrome, pfeiffer syndrome,  
jackson-weiss syndrome) (FGFR2) gene.

&lt;400&gt; 13

```

ccacctctgc tcggtgaaaa ttaagaaatt atgtgtaaga acagcattta gcaaatagct 60
attaaaaaaa gagagaccaa tttctag gt gcattgggac atccatttaa antcaatata 120
aaaaataact ccttgtaaat ntataatata ttatttatac ntaattt 167

```

&lt;210&gt; 14

&lt;211&gt; 414

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(414)

&lt;223&gt; 5' terminal sequence. fibroblast growth

factor receptor 2 (bacteria -expressed kinase,  
keratinocyte growth factor receptor, craniofacial  
dysostosis 1, crouzon syndrome, pfeiffer syndrome,  
jackson-weiss syndrome) (FGFR2) gene.

&lt;400&gt; 14

```

ggacacagaa tggataagcc agccaactgc accaacgaac tgtacatgat gatgagggac 60
tgttggcatg cagtgcctcc cagagaccaa cgttcaagca gttggtagaa gacttggatc 120
gaattctcac tctcacaacc aatgaggaat acttggaact cagccaacct ctggaacagt 180
attcacctag ttaccttgac ac aagaagtt cttgttcttc aggagatgat tctgtttttt 240
ctccagaccc catgccttac gaaccatgcc ttctcagta tccacacata aacgggcagt 300
gttttaaaac atgaatgact gtgtctggcc tgnccccaa acagggacag gcactggggg 360
aacctaggct acattnagga aggggaggac cttgccttc ccaggngttt gttt 414

```

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<210> 15  
<211> 4667  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(4667)  
<223> fibroblast growth factor receptor 2  
(bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, crouzon syndrome, pfeiffer syndrome, jackson-weiss syndrome) (FGFR2) gene.

<400> 15  
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&lt;210&gt; 16

&lt;211&gt; 483

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(483)

<223> 3' terminal sequence. ests (EST T89980)  
gene.

&lt;400&gt; 16

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ctg

483

<210> 17  
<211> 400  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(400)  
<223> 3' terminal sequence. protein phosphatase 3  
(formerly 2b), catalytic subunit, gamma isoform  
(calcineurin a gamma) (PPP3CC) gene.

<400> 17  
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tttccaataa taaataaata gaatttggtt ttgagtttta gatccacctg agccacggca 180  
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cattcgctca ttaattcggg ccagncct cgcgctttct ttcaaaactc cgggatcttg 360  
tgcntggagg cgaggnaccc ctctgatggg cttcccgggg 400

<210> 18  
<211> 490  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(490)  
<223> 5' terminal sequence. protein phosphatase 3  
(formerly 2b), catalytic subunit, gamma isoform  
(calcineurin a gamma) (PPP3CC) gene.

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gnttaggttc 490

<210> 19  
<211> 2134  
<212> DNA/RNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(2134)

<223> protein phosphatase 3 (formerly 2b),  
catalytic subunit, gamma isoform (calcineurin a  
gamma) (PPP3CC) gene.

<400> 19

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<210> 20

<211> 248

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(248)

<223> 3' terminal sequence. ests (EST T90726)  
gene.

14/292

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aaaaacca 248

<210> 21  
<211> 427  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(427)  
<223> 5' terminal sequence. ests (EST T90726)  
gene.

<400> 21  
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aactcactgt gagattgctg ttgatttgaa ggggtgcttc actaaggta tattttaag 180  
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aaactggcta tgggtagga aatg atgtta aanttatgtg gggaaagttt ttcccctccn 360  
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cctttga 427

<210> 22  
<211> 294  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(294)  
<223> 3' terminal sequence. sry (sex determining  
region y)-box 4 (SOX4) gene.

<400> 22  
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atccatttca gtttgaccgt gaacccctt ccagttcgtg tcctcctccg cccccgccc 240  
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<210> 23  
<211> 362  
<212> DNA  
<213> Artificial Sequence

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&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(362)

&lt;223&gt; 5' terminal sequence. sry (sex determining region y)-box 4 (SOX4) gene.

&lt;400&gt; 23

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cc
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362

&lt;210&gt; 24

&lt;211&gt; 2797

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2797)

&lt;223&gt; sry (sex determining region y) -box 4 (SOX4) gene.

&lt;400&gt; 24

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ttgtctgcac cccagcaag aaggcgagt agttttctag agacttgaag gactctcccc 2220
cttcctgcat caccaccttg gttttgtttt attttgcttc ttggtcaaga aaggaggga 2280
gaaccagcg caccctctcc cccctttttt taaacgcgtg atgaagacag aaggctccg 2340
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gcaggcgaat tccggtttg ggcc ttttt tcttccctct tttcccttg cccctctgc 2460
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cggcggtgc tgggcctcg cttcttttc tacgtgaaat cagtgggtg agacttcca 2700
gaccccgag gcgtggagga gaggagactg tttgatgtg tacaggggca gtcagtggag 2760
ggcgagtgtg ttcggaaaa aaaaagaaa aaaagg 2797

```

&lt;210&gt; 25

&lt;211&gt; 352

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(352)

<223> 5' terminal sequence. ring finger protein 5  
(RNF5) gene.

&lt;400&gt; 25

```

acggggggcc caacnanant cgcgagcngg gcgtggcggg cgcgaccttc gaatgt anta 60
tatgtttgga gactgctcgg gaagctgttg tcagtgtgtg tggccacctg tactgttggc 120
catgtcttca tcagtggctg gagacacggc cagaacggca agagtgtcca gtatgtaaag 180
ctgggatcag cagagagaag gttgtccgc tttatgggcg agggagccag aagccccagg 240
atcccagatt aaaaactcca cccgcccc aggcc agaga ccagctccg agagcagagg 300
gggattccag ccatittgtg atacggggg cttccaactn ttcatttggg gt 352

```

&lt;210&gt; 26

&lt;211&gt; 543

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(543)

&lt;223&gt; ring finger protein 5 (RNF5) gene.

&lt;400&gt; 26

```

atggcagcag cggaggagga ggacggggc cccgaaggc caaatcgca gcggggcggg 60
gcgggcgcga cttcgaatg taatatatgt ttggagactg ctcgggaagc tgtgtcagt 120

```

17/292

```

gtgtgtggcc acctgtactg ttggccatgt cttcatcagt ggctggagac acggc cagaa 180
cggcaagagt gtccagtatg taaagctggg atcagcagag agaaggttgt cccgctttat 240
gggcgaggga gccagaagcc ccaggatccc agattaaaaa ctccaccccg cccccagggc 300
cagagaccag ctccggagag cagaggggga ttccagccat ttggtgatac cgggggcttc 360
cactttctcat ttggtgtttg tgcttttccc ttt ggctttt tcaccaccgt cticaatgcc 420
catgagcctt tccgccgggg tacagggtg gatctgggac agggtcaccc agcctccagc 480
tggcaggatt ccctcttcct gtttctcgcc atcttcttct ttttttggct gctcagtatt 540
tga
543

```

&lt;210&gt; 27

&lt;211&gt; 397

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(397)

&lt;223&gt; 3' terminal sequence. axl receptor tyrosine kinase (AXL) gene.

&lt;400&gt; 27

```

gccgtggggt gggaaagtgg gaag gtggag ttttccccag tggcagtgt tagcttggat 60
cctgagaggg agtaccaggt ggagggttgt ctcaggcacc atcctcctgc cctgggctgc 120
tggggagccc ctatcagcag gctgagcggg gctaggggtt ttggaagggc agaggacata 180
gntccagca ggatggacct cagccgcagt naggcagcta caggaatcct taggggtctg 240
ctgggttggg gggtcagetc ctctgcagc tccaggggnt tcaggataac ctccaccctc 300
atccatntn acatagagga tttcgtcagg ctctggggc aggangcaan gcctttcagt 360
ntgttctcca aatcttccn caactctnta aaacttt
397

```

&lt;210&gt; 28

&lt;211&gt; 418

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(418)

&lt;223&gt; 5' terminal sequence. axl receptor tyrosine kinase (AXL) gene.

&lt;400&gt; 28

```

ctgaatgaga acatgtccgt gtgtgtggcg gacttcgggc tctccaagaa gatctaca at 60
ggggactact accgccagga ccgtatcgcc aagatgccag tcaagtggat tgccattgag 120
agtctagctg accgtgtcta caccagcaag agcgatgtgt ggtccttcgg ggtgacaatg 180
tgggagattg ccacaagagg ccaaacccca tatccggggc gtggagaaca gcgagattta 240
tgantatctg cgccagggaa atgcctgaa gcagcct ncg gactgtcttg gatgggantg 300
ttatgccttg atgttcgcgg tncctgggga gcttaaattc cccaggggnc ccgnccaatt 360
ttttacaaag cttncgggga agatttttgg gagnacacac ttttaagggc tttncctt 418

```

&lt;210&gt; 29

&lt;211&gt; 5015

&lt;212&gt; DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(5015)

<223> axl receptor tyrosine kinase (AXL) gene.

<400> 29

```
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ccagatagag agacacggcc tcaactggctc agcaccaggg tccccttccc cctcctcagc 120
tccctcctctg gcccttttaa gaaagagctg atcctctcct ctcttgagtt aaccctgat 180
tgtccagggtg gcccttggtc ctggcctggt gggcggaggc aaagggggag ccaggggagg 240
agaaagggtt gcccaagtct gggagtgagg gaaggaggca ggggtgctga gaaggcggct 300
gctgggcaga gccggtggca agggcctc cc ctgccgctgt gccaggcagg cagtgcctaaa 360
tccggggagc ctggagctgg ggggagggcc ggggacagcc cggcccgtctg cccctcccc 420
cgctgggagc ccagcaactt ctgaggaaag ttggcaccac atggcgctggc ggtgccccag 480
gatgggcagg gtcccgtctg cctggtgctt ggcgctgtgc ggctgggctg gcatggcccc 540
caggggcacg caggctgaag aaagtccctt cgtgggcaac ccagggaata tcacaggtgc 600
ccggggactc acgggcaccc ttccgtgtca gctccagggt caggagagc ccccgagggt 660
acattggctt cgggatggac agatcctgga gctcgcggac agcaccaga cccaggtgcc 720
cctgggtgag gatgaacagg atgactggat agtggtcagc cagctcag aa tcacctccct 780
gcagctttcc gacacgggac agtaccagtg ttggtgttt ctgggacatc agacctctgt 840
gtcccagcct ggctatgttg ggctggaggg ctgccttac ttctggagg agcccgaaga 900
caggactgtg gccgcaaca ccccttcaa cctgagctgc caagctcagg gacccccaga 960
gcccgtggag ctactctggc tccagg atgc tgtccccctg gccacggctc caggtcacgg 1020
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ccataacgcc aagggggtca ccacatcccg cacagccacc atcacagtgc tccccagca 1140
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gaaggccttg cctcctgccc aggagcctga cgaatcctc tatgtcaaca tggat gaggg 2940
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```

19/292

```
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tgagccaatc cctcaccttc tgagtacaga gtgtggactc tgggtgcctcc agaggggctc 4980
aggtcacata aaactttgta tatcaacgaa aaaaa 5015
```

&lt;210&gt; 30

&lt;211&gt; 439

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(439)

<223> 5' terminal sequence. cathepsin b (CTSB)  
gene.

&lt;400&gt; 30

```
aacacgtcac cggagagatg atgggtggcc atgcatccgc atcctgggct ggggagtgga 60
gaatggcaca cctactggc tgg ttgcaa ctctggaa actgactggg gtgacaatgg 120
cttctttaaa tactcagag gacaggatca ctgtggaatc gaatcagaag tgggtggctgg 180
aattccacgc accgatcagt actgggaaaa gatctaattc gccgtgggcc tgtcgtgcc 240
gtcctggggg gcgagatcgg ggtagaaatg cattttatc ttttaagtca cgttaaggat 300
acaagtttc agacagggtc tgaaagggan tgggatttng gccaaacatc agacctgttc 360
tttccaaggg gaggaccaag ttctggggct aacattcccc agcctnttgg ttttaacagtt 420
gncaggacag ggcntgtt 439
```

20/292

<210> 31  
<211> 1996  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(1996)  
<223> cathepsin b (CTSB) gene.

<400> 31  
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gcgatctggt tcccacctca gctcccgag tagtggatct aggatccggc ttccaacatg 180  
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cagggtcctt gtggctcctg ctgggccttc ggggctgtgg aagccatct c tgaaccggtc 540  
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tactccatcc ctccctgtga gcaccac gtc aacggctccc ggcccccatg caccggggag 780  
ggagatacc ccaagtgtag caagatctgt gagcctggct acagcccagc ctacaaacag 840  
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agttcccca gtacctcaa gcaagtagct ttccacattt gtcacagaaa tcagagga ga 1620  
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tttgagatt gcctccta at gacgcggctc aa aaggaaac caagtgtgca ggagttgttt 1860  
ctgacccact gatctctact accacaagga aaatagttaa ggagaaacca gcttttactg 1920  
tttttgaaaa attacagctt caccctgtca agttaacaag gaatgcctgt gccataaaaa 1980  
ggtttctcca acttga 1996

<210> 32  
<211> 492  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(492)

21/292

<223> 3' terminal sequence. protein phosphatase 4  
(formerly x), catalytic subunit (PPP4C) gene.

<400> 32

```
ttocattttt cttcttttat tagaattttt tcattttttt tctcaaaatt tttatctaaa 60
aacaacaga aaaaagaag aaaaaaagaa aaaaaaatta ttggaaactt catggttcaa 120
gtggggagag aggaggagga acatggagct aggtctccag gcctctccag agaagtcctc 180
accctcgaag caccctcttg ggggacagca gagccagg ga cagccccccc ccacgcccag 240
cctccgtctg aggggaagatg ggcagagtca cagtgggtgc gaggggccag aagggttggg 300
aggngggcag gggcgggcgg ggtcacagga agtagttcgg ccacggcttt ctttgggagg 360
gggatncccc gtgtcttctt ttgggggagc agccttcaaa gatgatgaaa tctttttctt 420
gggagatgct tcgttc cagc ttnccaagat tggcttncca cattttocca cagcgggtaca 480
agttagtttt tg 492
```

<210> 33

<211> 330

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(330)

<223> 5' terminal sequence. protein phosphatase 4  
(formerly x), catalytic subunit (PPP4C) gene.

<400> 33

```
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ctggcactta aggttcgcta tctgatcgc atcacactga tccgggg caa ccatgagagt 120
cgccagatca cgcaggtcta tggcttctac gatgagtgc tgcgcaagta acggctcggg 180
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tngaaagaat cttctgcgtg cacgggggcc tctccccctc catccagacc ctgggatcca 300
gattcggaca atcgaccgaa agcaa gaggt 330
```

<210> 34

<211> 1429

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(1429)

<223> protein phosphatase 4 (formerly x),  
catalytic subunit (PPP4C) gene.

<400> 34

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gagggggcgg cggccccgac tctgaccgc gccgggggtg ggccatggcg gagatcagcg 120
acctggaccg gcagatcgag cagctgcgtc gctgcgagct catcaaggag agcgaagtca 180
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tcagagtagg tggcgacgtc cctgagacca actacctctt catgggggac tttgtggacc 360
gtggcttcta tagcgtcgaa acgttcctcc tgctgctggc acttaaggt t cgctatcctg 420
atcgcatcac actgatccgg ggcaaccatg agagtcgcca gatcacgcag gtctatggct 480
```

22/292

```
tctacgatga gtgcctgcgc aagtaagggt cgggtgactgt gtggcgctac tgcactgaga 540
tcttttacta cctcagcctg tcagccatca tcgatggcaa gatcttctgc gtgcacgggg 600
gcctctcccc ctccatccag accctgg atc agattcggac aatcgaccga aagcaagagg 660
tgccatcatga tgggcccattg tgtgacctcc tctgggtctga cccagaagac accacaggct 720
ggggcgtgag cccccgagga gccggctacc tatttggcag tgacgtggtg gccagttca 780
acgcagccaa tgacattgac atgatctgcc gtgcccacca actggtgatg gaaggttaca 840
agtggcactt caatgagacg gtgctcactg tgtggtcggc acccaactac tgctaccgct 900
gtgggaatgt ggcagccatc ttggagctgg acgagcatct ccagaaagat ttcacatct 960
ttgaggctgc tccccaaagag acacggggca tcccctccaa gaagcccgtg gccgactact 1020
tctgtgacc ccgcccggcc cctgcccctt ccaacccttc tggccc tcgc accactgtga 1080
ctctgccatc ttctcagac ggaggctggg cgtggggggg gctgtcctgg ctctgctgtc 1140
ccccaagagg gtgcttcgag ggtgaggact tctctggaga ggcctggaga cctagctcca 1200
tgttctctct cctctctccc caattgaacc atgaagtttc caataatttt tttttctttt 1260
tttcttctt ttttctgttt gtttttagat aaaaattttg agaaaaaaa tgaaaaaatt 1320
ctaataaaag aagaaaaaatg aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1380
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1429
```

&lt;210&gt; 35

&lt;211&gt; 493

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(493)

<223> 3' terminal sequence. ests (EST T79867)  
gene.

&lt;400&gt; 35

```
tttttttggc acttcagctc caaaggtgaa acggcacagt taaaagcaag aaattttgtg 60
tcccttcccc aagctagctt tggaa taaat ccacttttct tgtaccagac cccactcttg 120
ttaattggac tctacatgtg gnaagcaact aacttgattt tcggttacaa tataatattc 180
aacttcagta aatcaaagac aattttgaaa gaagccaaag ggaaaaaaat gacctgaaga 240
gtcctgttta anttttagatt tctgaacaca aatctctggc gactaggact gaagcttgac 300
ctnttcttac ccaggaccn ttcccacctc actagggnac tttggantgg gatatatgtg 360
gggaaactct tgggctttcc ccattgtggc accatttcat atcttatggc aaatggtgcc 420
tcctacctcc cttgggnac tcccngttg gatgggtntt gggggaggag noctgntggg 480
gntttttccc at 493
```

&lt;210&gt; 36

&lt;211&gt; 354

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(354)

<223> 3' terminal sequence. fibroblast growth  
factor receptor 4 (FGFR4) g ene.

&lt;400&gt; 36

```
tttttgtttt ttatttcaaa aaaataattt ataaaacgcc atttgctcct gttttcggca 60
ggcttccagc ttctctgggc tcaggggcaa tgctcccgtc aagacgctgg ggcagcagca 120
```

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gcagggggag gtntggggaa aggggggttca gaggcccaga acctcctgct ggtattggga 180  
ggcaggaggt ttagcatagc agctctcca g ccaggctcag ccaaaccg gatggggact 240  
aagcgccaag gtccaagaag ccgagcagaa ccctgacatt tggggccatc aggacanagg 300  
cacggcagct cccaagggca aggggcacgg ccttngggac angggcacag caac 354

<210> 37  
<211> 336  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(336)  
<223> 5' terminal sequence. fibroblast growth  
factor receptor 4 (FGFR4) gene.

<400> 37  
atcggatgga ccgaccccc cactgcccc cagagctgta cgggctgatg cgtgagtgt 60  
ggcagcagcg ccctcccaga ggcctacctt caagcagctg gtggaggcgc tggacaagg 120  
ctgctggccg tctctgagga gtacctcgac ctccgctga ccttcggacc ctattcccc 180  
tctggtgggg aacgccagca gcacctgctt cctccagcga ttctgtcttc agccacgacc 240  
ccctgccatt ggggattcag ctcttccct ttgggtctng ggtgacagac atga gcaagg 300  
ctnaagggtt ttgcaaggga catagggttg gtgggc 336

<210> 38  
<211> 3015  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(3015)  
<223> fibroblast growth factor receptor 4 (FGFR4)  
gene.

<400> 38  
ccgaggagcg ctcggtgtgt ctgcggaccc tgccgcgtgc aggggtcgcg gccggctgga 60  
gctgggagtg aggcggcgga ggagccaggt gaggaggagc caggaaggca gttggtggga 120  
agtccagctt gggtcctga gagctgtgag aaggagatgc ggctgctgct gg ccctgttg 180  
ggggtcctgc tgagtgtgcc tggcctcca gtctgtccc tggaggcctc tgaggaagt 240  
gagcttgagc cctgcctggc tccagcctg gagcagcaag agcaggagct gacagtagcc 300  
cttgggcagc ctgtgcggct gtgctgtggg cgggctgagc gtggtggcca ctggtacaag 360  
gagggcagtc gcctggcacc tgctggcct gtacggggt ggaggggccc cctagagatt 420  
gccagcttcc tacctgagga tgctggcgc tactctgcc tggcagcagg ctccatgac 480  
gtcctgcaga atctcacctt gattacaggt gactcctga cctccagcaa cgatgatgag 540  
gaccccaagt cccataggga cctctogaat aggcacagtt acccccagca agcaccctac 600  
tgacacaccc cccagcgcat ggagaagaaa ctgcatgcag tactgcccgg gaacaccgtc 660  
aagttccgct gtccagctgc aggcaacccc acgcccacca tccgctggct taaggatgga 720  
caggcctttc atggggagaa ccgcattgga ggcattcggc tgcgccatca gcaactggag 780  
ctcgtgatgg agagcgtggt gccctgggac cgcggcacat acacctgcct ggtagagaac 840  
gctgtgggca gcatccgcta taactacctg ctgatgtgc tggagcggtc cccgcaccgg 900  
cccatcctgc aggcggggt cccggccaac accacagccg tgggtggcag cgacgtggag 960  
ctgctgtgca aggtgtacag cgatgcccag cccacatcc agtggctgaa gcacatcgtc 1020



24/292

```

atcaacggca gcagcttcgg agccgacg gt tccccctatg tgcaagtcct aaagactgca 1080
gacatcaata gctcagaggt ggaggtcctg tacctgcgga acgtgtcagc cgaggacgca 1140
ggcgagtaca cctgcctcgc aggaattcc atcggcctct cctaccagtc tgcttggtc 1200
acggtgctgc cagaggagga ccccatatgg accgcagcag cggccgaggc caggatatac 1260
gacatcatcc tgtacgcgtc gggctccctg gccttggtg tgctcctgct gctggccggg 1320
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ctctcccgtc tccctctggc ccgacagttc tccctggagt caggctcttc cggcaagtca 1440
agctcatccc tggtagcagg cgtgcgtctc tccctcagcg g ccccgctt gctgcggcg 1500
ctcgtgagtc tagatctacc tctcgacca ctatgggagt tcccccgga caggctggtg 1560
cttgggaagc ccctagcgga gggctgctt ggccaggtag tacgtgcaga ggcctttggc 1620
atggaccctg cccggcctga ccaagccagc actgtggccg tcaagatgct caaagacaac 1680
gcctctgaca aggacc tggc cgacctggtc tcggagatgg aggtgatgaa gctgatcggc 1740
cgacacaaga acatcatcaa cctgcttggg gtctgcaccc aggaagggcc cctgtacgtg 1800
atcgtggagt gcgcgcgcaa gggaacctg cgggagttcc tgcggggccg gcgcccccca 1860
ggccccgacc tcagcccgga cgtcctcgg agcagtggg ggcgctctc ctcc cagtc 1920
ctggtctcct gcgcctacca ggtggccga ggcattgcagt atctggagtc ccggaagtgt 1980
atccaccggg acctggctgc ccgcaatgt ctggtgactg aggacaatgt gatgaagatt 2040
gctgactttg ggctggcccg cggcgtccac cacattgact actataagaa aaccagcaac 2100
ggccgcctgc ctgtgaagtg gatggcggc gaggcctgt ttgaccgggt gtacacacac 2160
cagagtgaag tgtgttcttt tgggacctg ctatgggaga tcttcaccct cgggggctcc 2220
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gaccaccccc cacactgccc cccagagctg tacgggctga tgcgtgagtg ctggcacgca 2340
gcgcctctcc agaggcctac cttcaagcag ctggtggagg cgttggaaca ggtcctgctg 2400
gcgctctctg aggagtacct cgacctcgc ctgaccttcg gacctatc cccctctggt 2460
ggggacgcca gcagcactg ctctccagc gattctgtct tcagccacga cccctgcca 2520
ttgggatcca gtccttccc cttcgggtct ggggtgcaga cat gagcaag gctcaaggct 2580
gtgcaggcac ataggctggg gcccttggg cttggggctc agccacagcc tgacacagt 2640
ctcgaccttg atagcatgg gccctggc cagagttgct gtgcccgtgc caaggccgt 2700
gcccttggc ttggagctgc cgtgcctgt tctgtatgg ccaaatgtca gggttctgct 2760
cggcttcttg gaccatgg cg cttagtcccc atcccgggt tggctgagcc tggctggaga 2820
gctgctatgc taaacctcct gcctccaat accagcagga ggttctggg ctctgaaccc 2880
cctttcccca cacctcccc tgcgtgctg gcccagcgt cttgacggga gcattggccc 2940
ctgagcccag agaagctgga agcctgccga aaacaggagc aaatggcgt ttataaa tta 3000
tttttttgaa ataaa
3015

```

<210> 39  
 <211> 252  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(252)  
 <223> 3' terminal sequence. ectonucleotide  
 pyrophosphatase/phosphodiesterase 2 (autotaxin)  
 (ENPP2) gene.

```

<400> 39
gtgtgattta ttatgtttta gattggttta taaggcttaa atatatctgt catagttaac 60
agttaacagc aaataaaggc aactttacaa aatcagtgtt tccatacagt acaggactaa 120
atgtggcaac tgtgcattgg aaaattaata tttctcaat gcaaatntca aatctgcagc 180
accatttaga agcttccact aaaaactcaa gctgcagtat ttattacang ctctactcng 240
aacacanggc ta
252

```

<210> 40  
 <211> 382

25/292

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(382)

<223> 5' terminal sequence. ectonucleotide  
pyrophosphatase/phosphodiesterase 2 (autotaxin)  
(ENPP2) gene.

&lt;400&gt; 40

```
ctnacnttca aacgganntg gaa ttatttc caaagggtat tggatgaagaa atatgcttcg 60
gaaagaaatg gagttaacgt gataagtga ccaatcttcg actatgacta tgatggctta 120
catgacacag aagacaaaat aaaacagtac gtggaaggca gttccattcc tgttccaact 180
cactactaca gcatcatcac cagctgtctg gattttactc agcctgccga caagtgtgac 240
ggccctctct ctgtgtcctc cttcatcctg cctcaccggc ctgacaacga ggagagctgc 300
aatagctcag aggacgnatt caaatgggt agnaggaact catgaaggnt gcacacagct 360
agggtnctgt gacctttgna cc 382
```

&lt;210&gt; 41

&lt;211&gt; 2592

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2592)

<223> ectonucleotide  
pyrophosphatase/phosphodiesterase 2 (autotaxin)  
(ENPP2) gene.

&lt;400&gt; 41

```
atggcaagga ggagctcgtt ccagtcgtgt ca gataatat ccctgttcac ttttgccgtt 60
ggagtcataa tctgcttagg attcactgca catcgaatta agagagcaga aggatgggag 120
gaaggtcctc ctacagtgtc atcagactcc ccctggacca acatctccgg atcttgcaag 180
ggcaggtgct ttgaacttca agaggtgga cctcctgatt gtcgctgtga caacttgtgt 240
aagagctata ccagttgtct ccatgacttt gatgagctgt gtttgaagac agcccgctgc 300
tgaggagtga ctaaggacag atgtggggaa gtcagaaatg aagaaaatgc ctgtcactgc 360
tcagaggact gcttggccag gggagactgc tgtaccaatt accaagtgtt ttgcaaagga 420
gagtcgcatt gggttgatga tgactgtgag gaaataaagg ccgcagaatg ccc tgcaggg 480
tttgttcgcc ctccattaat catcttctcc gtggatggct tccgtgcac atacatgaag 540
aaaggcagca aagtcatgcc taatattgaa aaactaaggc cttgtggcac acactctccc 600
tacctagggc cgggtgaccc aactaaaacc tttcctaact tatacacttt ggccactggg 660
ctatatccag aatcacatgg aattgttggc a attcaatgt atgatcctgt atttgatgcc 720
acttttcatc tgcgagggcg agagaaatth aatcatagat ggtggggagg tcaaccgcta 780
tggtattacg ccaccaagca aggggtgaaa gctggaacat tcttttggtc tgttgcac 840
cctcacgagc ggagaatatt aaccatattg cagtggctca ccctgccaga tcatgagagg 900
ccttcggtct atgccttcta ttctgagcaa cctgatttct ctggacacaa atatggccct 960
ttcggccctg agatgacaaa tcctctgagg gaaatcgaca aaattgtggg gcaattaatg 1020
gatggactga aacaactaaa actgcatcgg tgtgtcaacg tcatcttgt cggagaccat 1080
ggaatggaag atgtcacatg tgatagaact gagttcttga gtaattacct aactaatgtg 1140
gatgatatta ctttagtgcc tggaaactcta ggaagaattc gatccaaatt tagcaacaat 1200
gctaaatatg accccaaagc cattattgcc aatctcacgt gtaaaaaacc agatcagcac 1260
tttaagcctt acttgaaaca gcaccttccc aaacgtttgc actatgccaa caacagaaga 1320
```

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```

attgaggata tccatttatt ggtg gaacgc agatggcatg ttgcaaggaa acctttggat 1380
gtttataaga aaccatcagg aaaatgcttt ttccagggag accacggatt tgataacaag 1440
gtcaacagca tgcagactgt tttttaggt tatggcccaa catttaagta caagactaaa 1500
gtgcctccat ttgaaaacat tgaactttac aatgttatgt gtgatctcct gggattgaag 156 0
ccagctccta ataatgggac ccatggaagt ttgaatcatc tcctgcgcac taataccttc 1620
aggccaacca tgccagagga agttaccaga cccaattatc cagggattat gtaccttcag 1680
tctgattttg acctgggctg cacttgtgat gataaggtag agccaaagaa caagttggat 1740
gaactcaaca aacggcttca taaaaaggg tctacaga ag agagacacct cctctatggg 1800
cgacctgcag tgctttatcg gactagatat gatattttat atcacactga ctttgaaagt 1860
ggttatagtg aaatattcct aatgccactc tggacatcat atactgtttc caaacaggct 1920
gaggtttcca gcgttcctga ccatctgacc agttgcgtcc ggctgatgt cgtgtttct 1980
ccgagtttca gt cagaactg tttggcctac aaaaatgata agcagatgtc ctacggattc 2040
ctctttcctc cttatctgag ctcttcacca gaggtctaat atgatgcatt ccttgtaacc 2100
aatatgggtc caatgtatcc tgctttcaaa cgggtctgga attatttcca aagggtattg 2160
gtgaagaaat atgcttcgga aagaaatgga gttacagtga taagtggacc a atcttcgac 2220
tatgactatg atggcttaca tgacacagaa gacaaaataa aacagtacgt ggaaggcagt 2280
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cctgccgaca agtgtgacgg ccctctctct gtgtcctcct tcactcctgcc tcaccggcct 2400
gacaacgagg agagctgcaa tagctc agag gacgaatcaa aatgggtaga agaactcatg 2460
aagatgcaca cagctagggt gcgtgacatt gaacatctca ccagcctgga cttcttccga 2520
aagaccagcc gcagctaccc agaaatcctg acactcaaga catacctgca tacatatgag 2580
agcgagattt aa 2592

```

&lt;210&gt; 42

&lt;211&gt; 467

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(467)

<223> 3' terminal sequence. v-rel avian  
reticuloendotheliosis viral oncogene homolog a  
(nuclear factor of kappa light polypeptide gene  
enhancer in b-cells 3 (p65)) (RELA) gene.

&lt;400&gt; 42

```

acagatttat tagttcagag tagaaagagc aagagtccaa gtgctttgat tgttcagtaa 60
aaactatgcc tcnngactgg agagctgcca gcctgctctc cccactctt aacaacttac 120
cctactatta aggcaattga gaagagggag agcaaggaag tcccagacca aacccttct 180
ggatecnngg ngagagccag tgctgttgcn tggntttcct tcagccatgg ttgagcaagg 240
aaagagcccg cagagacctc ttagggcag gaaggccagc ccctcaaagc ctggtnttag 300
ggcacagggg acaatgccag tgccatacag gggctggtat ctgggggcgt tattttgatt 360
aagctgtaat gaatccatga tgggaaggac acttgataag gctttntggg gctcaaaggn 420
ctttacctcc agcctgcttc tntctctagg gngagtaccc agaagct 467

```

&lt;210&gt; 43

&lt;211&gt; 2444

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

27/292

&lt;222&gt; (1)..(2444)

<223> v-rel avian reticuloendotheliosis viral  
oncogene homolog a (nuclear factor of kappa light  
polypeptide gene enhancer in b-cells 3 (p65))  
(RELA) gene.

&lt;400&gt; 43

```
ggcagcaggc ggggccgggt cgcagctggg cccgcggcat ggaagaaactg ttccccctca 60
tcttccccgc agagcagccc aagcagcggg gcatgcgctt ccgctacaag tgcgaggggc 120
gctccgcggg cagcatccca ggcgagagga gcacagatac caccaagacc caccaccacca 180
tcaagatcaa tggctacaca ggaccaggga cagtgcgcat ctccctggtc a ccaaggacc 240
ctctcaccg gcctcaccgc cagcagcttg taggaaagga ctgccgggat ggcttctatg 300
aggctgagct ctgcccggac cgctgcatcc acagtttcca gaacctggga atccagtgtg 360
tgaagaagcg ggacctggag caggctatca gtcagcgcac ccagaccaac aacaacccct 420
tccaagttcc tataagaag cagcgtgggg actacgacct gaatgctgtg cggctctgct 480
tccaggtgac agtgcgggac ccacaggca ggccccctcg cctgcgcgct gtcctttctc 540
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gaaactcttg cagctgcctc ggtggggatg agatcttctt actgtgtgac aaggtgcaga 660
aagaggacat tgaggtgtat ttcacgggac caggctggga ggcccagggc tccttttctc 720
aagctgatgt gcaccgacaa gtggccattg tgttccggac ccctccctac gcagacccca 780
gcctgcaggc tcctgtgcgt gtctccatgc agctgcggcg gccttccgac cgggagctca 840
gtgagcccat ggaattccag tacctgccag atacagacga tgcacaccg attgaggaga 900
aacgtaaaag gacatatgag accttcaaga gcatcatgaa gaagatcct ttcagcggac 960
ccaccgaccc ccggcctcca cctcgacgca ttgctgtgcc ttccgcgac tcagcttctg 1020
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cagctctggc ccaggcccca gccctgtcgc cagctcagc cccaggccct cctcaggctg 1260
tggccccacc tgcgcccaag cccacccagg ctggggaagg aacgctgtca gaggccctgc 1320
tgcagctgca gtttgatgat gaagacctgg gggccttgct tggcaacagc acagaccag 1380
ctgtgttcac agacctggca tccgtcgaca actccgagtt tcagcagctg ctgaaccagg 1440
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ctcgccctag gacagcccag agggcccccg accagctcc tgctccactg ggggcccccg 1560
ggctcccaaa tggcctcctt tcaggagatg aagacttctc ctccattgag gacatggact 1620
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gtctctgcg gctctttcct tgctcaac ca tggctgaagg aaacagtga acagcactgg 2220
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caggaggcat agtttttagt gaacaatcaa agcacttgga ctcttgctct ttctactctg 2400
aactaataaa gctgttgcca agctggacgg cagcagctcg tgcc 2444
```

&lt;210&gt; 44

&lt;211&gt; 381

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(381)

28/292

<223> 5' terminal sequence. il2 -inducible t-cell  
kinase (ITK) gene.

<400> 44

```
aactctttcc tttggttggtg ctaagagggtg atgcccgaag tgcaccacct ttcaagaact 60
ggatcatgaa caactttatc ctcttggaag aacagctcat caagaaatcc caacaagaga 120
agaacttctc cctcgaactt taaagtccgc ttcttttggt taaccaaagc cagcctgg ca 180
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<211> 6381

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(6381)

<223> il2-inducible t-cell kinase (ITK) gene.

<400> 45

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&lt;213&gt; Artificial Sequence

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&lt;220&gt;

&lt;221&gt; misc\_feature

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&lt;223&gt; 5' terminal sequence. tenascin xb (TNXB) gene.

&lt;400&gt; 46

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&lt;223&gt; tenascin xb (TNXB) gene.

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34/292

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&lt;210&gt; 48

&lt;211&gt; 438

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(438)

<223> 3' terminal sequence. colony stimulating  
factor 1 (macrophage) (CSF1) gene.

&lt;400&gt; 48

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tcacagtgcg tgancaatgt cctctc ttga cttctcagag aacagaaggg gttcctgagc 180
aggtagcctg gggggacacc agagngcct ctggggctcc tcctgctctg atgccaccaa 240
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tatgtttaag gtaggggggg atgaaggggg gaatgccctt tttatttttc ttccattttt 360
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ccctttgccca ggttcact

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438

&lt;210&gt; 49

&lt;211&gt; 390

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(390)

<223> 5' terminal sequence. colony stimulating factor 1 (macrophage) (CSF1) gene.

<400> 49

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ggggangggc ttccattttn tggggccagc 390
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<210> 50

<211> 2475

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(2475)

<223> colony stimulating factor 1 (macrophage) (CSF1) gene.

<400> 50

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36/292

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tatcaatttg cactt                                     2475

```

&lt;210&gt; 51

&lt;211&gt; 397

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(397)

<223> 3' terminal sequence. villin 2 (ezrin)  
(VIL2) gene.

&lt;400&gt; 51

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ccactggtcc ctggttaagtt tgtgtggtc catcactctt tgagggatca nccgctcaga 180
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tcctttcctt cacttnggag ggaggaaaag tttctggggt gatgtcctgg ggatgagctt 360
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```

&lt;210&gt; 52

&lt;211&gt; 468

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(468)

<223> 5' terminal sequence. villin 2 (ezrin)  
(VIL2) gene.

&lt;400&gt; 52

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```

37/292

gttccggggc caagttctac cctgaagatg tgggctgagg agctcattcc agggacattc 420  
accagaaat tttntttcnt ccaagtgaag gaagggattc ttaggcgn 468

&lt;210&gt; 53

&lt;211&gt; 3064

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(3064)

&lt;223&gt; villin 2 (ezrin) (VIL2) gene.

&lt;400&gt; 53

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&lt;211&gt; 435

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

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<223> 3' terminal sequence. adenomatosis polyposis  
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&lt;210&gt; 55

&lt;211&gt; 414

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

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<223> 5' terminal sequence. adenomatosis polyposis  
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 ataatttct ctttcttaat attatagaaa ttctgtactt gaaattgatt cttagacatt 9840  
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 gtataatcag actttgccat gctcagaaaa ttcaaatcac atggaacttt agaggtagat 10020  
 ttaatacgat taagatatc agaagtatat tttagaatcc ctgcctgtta aggaaacttt 10080  
 atttctggta ggtacagtc tgggtacat gttaaagtgc ccttatata gtggaggga 10140  
 gtcttccttc ctgaaggaata ataaactgac acttattaac taagataatt tacttaatat 10200

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atctnccctg atttgtttta aaagatcaga ggggtgactga tgatacatgc atacatatatt 10260  
 gttgaataaa tgaaaattta ttttttagtga taagattcat acactctgta tttggggaga 10320  
 gaaaaccttt ttaagcatgg tggggcactc agataggagt gaatacacct acctggtggt 10380  
 cat 10383

&lt;210&gt; 57

&lt;211&gt; 404

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(404)

<223> 5' terminal sequence. mucin 1, transmembrane  
(MUC1) gene.

&lt;400&gt; 57

aaacggaagc agcctctoga tataacctga cgatctcaga cgtcagcgtg agtgatgtgc 60  
 catttccttt ctctgccag tctgggctg ggggtgccagg ctggggcacc gcgtgctgg 120  
 tgctggtctg tgttctggtt gcgctggcca ttgtctatct cattgccttg gctgtctgtc 180  
 agtgccgccc aaagaactac gggcagctgg acatctttcc ag cccgggat acctaccatc 240  
 ctatgagcga gtacccacc taccacacc atggggcgct atgtgcccc taggcagtac 300  
 cgatcgtagc ccctatgaga aggttttng caggtaatng gttggcagca gcttttttta 360  
 caaaaaacc aggagctngg cagccatttt tgtccaattt ttag 404

&lt;210&gt; 58

&lt;211&gt; 1721

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1721)

&lt;223&gt; mucin 1, transmembrane (MUC1) gene.

&lt;400&gt; 58

gaattccctg gctgcttgaa tctgttctgc ccctcccca ccatttcac caccaccat g 60  
 acaccgggca ccagtcctcc tttcttctg ctgctgtcc tcacagtgt tacagttgtt 120  
 acaggttctg gtcagtcaag ctctaccca ggtggagaaa aggagacttc ggctaccag 180  
 agaagttcag tgcccagctc tactgagaag aatgctgtga gtatgaccag cagcgtactc 240  
 tccagccaca gcccgggttc aggtcctcc accactca gg gacaggatgt cactctggcc 300  
 ccggccacgg aaccagcttc aggttcagct gccacctggg gacaggatgt cacctcggtc 360  
 ccagtcacca ggccagccct gggctccacc accccgccag cccacgatgt cacctcagcc 420  
 ccggacaaca agccagcccc gggctccacc gccccccag cccacgggtgt cacctcggcc 480  
 ccggacacca ggccgcccc gggctccacc gccccccag cccacgggtgt cacctcggcc 540  
 ccggacacca ggccgcccc gggctccacc gggccgcag cccacgggtgt cacctcggcc 600  
 ccggacacca ggccgcccc gggctccacc gccccccag cccatgggtgt cacctcggcc 660  
 ccggacaaca ggcccgctt ggcgtccacc gcccctccag tccacaatgt cacctcgg cc 720  
 tcaggctctg catcaggctc agcttctact ctggtgcaca acggcacctc tgccagggt 780  
 accacaaccc cagccagcaa gagcactcca ttctcaattc ccagccacca ctctgatact 840  
 cctaccaccc ttgccagcca tagcaccagg actgatgcca gtagcactca ccatagcacg 900  
 gtacctctc tcacctctc caatcacagc acttct cccc agttgtctac tggggtctct 960  
 ttctttttcc tgtcttttca catttcaaac ctccagttta attcctctct ggaagatccc 1020

43/292

```

agcaccgact actaccaaga gctgcagaga gacatttctg aaatgttttt gcagatttat 1080
aaacaagggg gttttctggg cctctccaat attaagttca ggccaggatc tgtggtggta 1140
caattgactc tggccttcgg agaaggtacc atcaatgtcc acgacgtgga gacacagttc 1200
aatcagtata aaacggaagc agcctctcga tataacctga cgatctcaga cgtcagcgtg 1260
agtgatgtgc catttccttt ctctgcccag tctggggctg ggggtgccag ctgggggcac 1320
gcgctgctgg tctgtgtctg tgttctgggt gcgctggcca ttgtctatct cattgccttg 1380
gctgtctgtc agtgccgcg aaagaactac gggcagctgg acatctttcc agcccgggat 1440
acctaccatc ctatgagcga gtacccacc taccacacc atgggcgcta tgtgccccct 1500
agcagtaccg atcgtagccc ctatgagaag gttctgcag gtaatggtg cagcagcctc 1560
tcttacacaa acccagcagt ggcag cact tctgccaaact tgtaggggca cgtcgccctc 1620
tgagctgagt ggccagccag tgccattcca ctccactcag ggctctctgg gccagtcctc 1680
ctgggagccc ccaccacaac acttcccag catggaattc c 1721

```

<210> 59  
 <211> 359  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(359)  
 <223> 3' terminal sequence. insulin-like growth  
 factor 2 (somatomedin a) (IGF2) gene.

```

<400> 59
ttagccaatt gatttttttg gtggttgttt tttttaaagc caatttctga gcttttgtgg 6 0
ggtgtttcta aaaagccaat tagttttaag agggttgttg tggggggggg ggaagggggg 120
tagtttaatg ttttgatttt ttatgtgttg ggataatttg ggataatttg gggggagggg 180
atgtgaaggg tgtttaaagc caatcgattt tgtacatgtt tgaagatgct gctgtgcttc 240
ctcagcccga tggagggggc cgaggagagt agcctgtttc ggggaggcng ggcacgggga 300
ctgggtcang agaagcccca gggggaccgt ngaccccaga gattttcggg atggaaccc 359

```

<210> 60  
 <211> 410  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(410)  
 <223> 5' terminal sequence. insulin-like growth  
 factor 2 (somatomedin a) (IGF2) gene.

```

<400> 60
gtcgaccct ccgaccgtgc ttccggacaa ctccccaga taccctgtgg gcaagttctt 60
ccaatatgac acctgggaag cagtccacc agcgctcga ggggcnctgc ctgccctcct 120
gcgtgcccgc cggggtc acg tgctcgccaa ggagctcgag gcgttcaggg aggccaaacg 180
tcaccgtccc ctgattgtc taccaccca agaccccgcc cacggggcgc nccccccaga 240
gatgggccag caatcggaag tgagcaaat tgccgcaagt ntttcagccc ggcgncacca 300
ttccttgtag cttntntntt gaaccacgga gttttncttn aggtttccat tccngaaaa t 360
tttttngggt ttncaagttt cccttggggg gttttttttn tttgaaacca 410

```

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<210> 61  
<211> 1356  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(1356)  
<223> insulin-like growth factor 2 (somatomedin a)  
(IGF2) gene.

<400> 61  
ttctcccgca accttccctt cgtccctcc cgtcccccc agtccttagc ctccgactcc 60  
ctccccccct cagcgccgcc ctctcgctt cgccgaacca aagtggatta attacacgct 120  
ttctgtttct ctccgtgctg ttctctcccg ctgtgcgcc gcccgcctct cgtgtcctc 180  
tctccccctc gccctctctt cggccccccc ctttcacgtt cactctgtct ctcccactat 240  
ctctgcccc ctctatcctt gatacaacag ctgacctcat ttcccgatac cttttcccc 300  
ccgaaaagta caacatctgg ccgccccag ccgaagaca gccgctcctc cctggacaat 360  
cagacgaatt ctcccccccc cccaaaaa aa aaaagccatc cccccgctct gcccgctgc 420  
acattcgcc ccgcgactc ggccagagcg gcgtggcag aggagtgtcc ggcaggagg 480  
ccaacgccc ctgttcggtt tgcgacacgc agcaggagg tggcgccag cgtcgccggc 540  
ttccagacac caatgggaat cccaatggg aagtogatgc tgggtgctt caccctcttg 600  
gccttcgct cgtgctgcat tgcgtcttac cgtccagtg agaccctgt cggcggggag 660  
ctggtggaca cctccagtt cgtctgtgg gaccgcggt tctacttcag caggcccga 720  
agccgtgtga gccgtcgag ccgtggcatc gttgaggagt gctgtttccg cagctgtgac 780  
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cgccggggtc acgtgctgc caaggagctc gaggcgttca gggaggccaa acgtcaccgt 1020  
ccctgattg ctctacccac ccaag acccc gccacgggg gcgcccccc agagatggcc 1080  
agcaatcgga agtgagcaaa actgcccga gtctgcagc cggcgccacc atcctgcagc 1140  
ctctctctga ccacggacgt ttccatcagg ttccatccc aaaatctctc ggttccacgt 1200  
ccccctggg cttctctga ccagtcctc gtgccccgc tccccgaaac aggctactct 1260  
cctcgcccc ctccatggg ctgaggaagc acagcagcat cttcaaacat gtacaaaatc 1320  
gattggcttt aaacaccctt cacataccct ccccc 1356

<210> 62  
<211> 474  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(474)  
<223> 3' terminal sequence. egf-like module  
containing, mucin-like, hormone receptor-like  
sequence 1 (EMR1) gene.

<400> 62  
tttaggagna aatcagtcag acaggcgaca aatcatttat tgagaggttc tctgtgtcag 60  
gcgtatgata ggcgctggag ggcacgctt agaaccatgc accaacaagg gcaggagaaa 120  
acaaaatgg agccaggtgt tcttggtcat gccattgaat ttgggtctgt tctcagaaac 180  
tctggaattg aagaagttgc aganaccgaa gataaaatgg tcgtttggag cagaaacacc 240  
tgatttctca tcagtgcata caaccacagg aagacggccc ccaacatt ct tccccagagg 300

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gttctggggc tgggtgggga tccctcatTT cccatgttaa gcttgaggaa gagatttcag 360  
 ggtaggctcc ctgcaggga actacttgTc cctcaactTT nggcctccca tagcatattt 420  
 tnaaagccag naagggtttt ttaaccctt ntttggaag cccgattggc att 474

&lt;210&gt; 63

&lt;211&gt; 457

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(457)

<223> 5' terminal sequence. egf-like module  
 containing, mucin-like, hormone receptor-like  
 sequence 1 (EMR1) gene.

&lt;400&gt; 63

tctgtccaac ggccaggTac gagaagaata caagaggtgg atcactggga agacgaagcc 60  
 cagctcccag tcccagacct caaggatctt gctgtcctcc atgccatccg ctccaagac 120  
 gggTtaaagt cttttctTgc tttcaaatat gctatggagc cacagttgag gacagtagtt 180  
 tcctgcagga gcctaccctg aaatctcttc tcag cttaac atgggaaatg aggatccac 240  
 cagccccagg aaccctctgg gggaaggaat gttggggggc cgtcttcctg tgggttgat 300  
 tgcantgatg gaggaaatca ggtgtttttt gntccaaacg gaccatttta ntctttcgtg 360  
 gntttgcaan ttttttcaan ttccagagtt ttttgaggna caggacccaa nttcantggg 420  
 catgnaccag gaacatcggg gttaaccontt tttgttt 457

&lt;210&gt; 64

&lt;211&gt; 3149

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(3149)

<223> egf-like module containing, mucin-like,  
 hormone receptor-like sequence 1 (EMR1) gene.

&lt;400&gt; 64

ctaaagtTTt tttctttgaa tgacagaact acagcataat gcgtggcttc aacctgctcc 60  
 tcttctgggg atgttgTgtt atgcacagct gggaagggca cataagaccc acacggaaac 120  
 caaacacaaa gggtaataac tgtagagaca gtacctTgtg c ccagcttat gccacctgca 180  
 ccaatacggT ggacagttac tattgcactt gcaaacaagg cttcctgtcc agcaatgggc 240  
 aaaatcactt caaggatcca ggagtgcgat gcaaagatat tgatgaatgt tctcaaagcc 300  
 cccagccctg tggTcctaac tcctcctgca aaaacctgtc agggaggTac aagtgcagct 360  
 gtttagatgg tttctctTct cccactggaa atgactgggt cccaggaaaag cggggcaatt 420  
 tctcctgtac tgatatcaat gagtgcctca ccagcagggt ctgccctgag cattctgact 480  
 gtgtcaactc catgggaagc tacagtTgca gctgtcaagt tggattcatc tctagaaact 540  
 ccacctgtga agacgtgaat gaatgtgcag atccaagagc ttgccagag catgcaactt 600  
 gtaataacac tgttggaac tactctTgtt tctgcaaccc aggatttgaa tccagcagtg 660  
 gccacttgag ttgccagggt ctcaaagcat cgtgtgaaga tattgatgaa tgcactgaaa 720  
 tgtgccccat caattcaaca tgcaccaaca ctctggggag ctactttTgc acctgccacc 780  
 ctggctttTg accaagcagT ggacagttga atttcacaga ccaaggagtg gaatgtagag 840  
 atattgatga gtgccgcca gatccatcaa cctgtggTcc taattctatc tgcaccaatg 900

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ccctgggctc ctacagctgt ggctgcattg taggctttca tcccaatcca gaaggctccc 960
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ccgataataa gcagatc cag caatgccaaag aggggaaccgc agtgaaacct gcataatgtct 1080
ccttttctgc acaaataaat aacatcttca gcgttctgga caaagtgtgt gaaaaataaaa 1140
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cggttttaaa tgagcgttc ttccaagacc accaggctcc cttgaccacc tctgagatca 1560
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ccatctgtgt ttcttgaggc actgatgtga aggttggaa agggacatcc tttggctgtg 1740
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ccgttatcat ggcgtctggg gagctcacga tggactttc cttgtacatc attagccatg 1860
taggcattat catctccttg gtgtgcctcg tcttgccat cgcc acctt ctgctgtgtc 1920
gtccatccg aaatcacaa acctacctc acctgcacct ctgcgtgtgt ctctcttgg 1980
cgaagactct ctctctcgcc ggtatacaca agactgacaa caagacgggc tgcgccatca 2040
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tgatactgtt cttgatggt c agaaacctga aggtgtgaa ttacttcagc tctcgcaaca 2160
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cagggttcat ctggagttt ttggggccag tttgcacagt tatagtatc aactccct tc 2340
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cagacgttct tgctccaaac gacctttt tctctgtgt ctgcaactt tcaattcca 2940
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gcctgacaca gagaacctt caataaatga tttgtgcct gtctgactga tttaccctaa 3120
aaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3149

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&lt;210&gt; 65

&lt;211&gt; 412

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(412)

<223> 3' terminal sequence. k1aa0427 gene product  
(K1AA0427) gene.

&lt;400&gt; 65

```

ttaatatoga ctcgccaac atttacattt acatg gatgg acaggacgat ccccaaacag 60
tgaaggttta cagactgggtc aagggaaggac gaacagagag aatggggctc gaggggtcac 120
atcccgtgga ggggtggcggg gtccttggtc tgcgtgtggg gaggttggga gcctcgctgg 180
ggctgcggtc ccagagcttc ggcaaagcca ccaggccttg gggagcaggg ctttggcaaag 240
caggccgctt cgga gaaaaa caatgactaa ctcatcctga cagggcagtt ggggagactt 300
taggacaggn ttcaacattc agatgggctt ggaccncctt tttccattnc ggccaaggaa 360

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ccccggggcgn aggggngaaa gcaattncaa agccttttagg aaatttcaat tt

412

&lt;210&gt; 66

&lt;211&gt; 442

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(442)

<223> 5' terminal sequence. k1aa0427 gene product  
(K1AA0427) gene.

&lt;400&gt; 66

atctgaacaa caacacttta agctgttttt ctaaattgcag gttgctgctc ctttttcaga 60  
tatggaagga aaacgttaag actatttttt ttttaaagaa acaacagtca agcctaaaaat 120  
ttgagacccc gaggcagctt cccgagggag actgtctcaga caggaactgc aggacagaag 180  
tggatgcccc acagaccctg ggccccctcc ccaagtccat cccctctctg tgggcatgag 240  
gaaggccgcg tccgagttga cctctgaatg tatgtgatga gaggcagagc tgggatattg 300  
catttcttaa gggttgcatt gcttttcccc ttccgcccgcg ttctttggcg catggaagga 360  
ggcggttcca gccatcttga tgttgatcc ngttttcagt nttccccant tgcctnttca 420  
gggatngagt tagttcattt tt 442

&lt;210&gt; 67

&lt;211&gt; 5737

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(5737)

&lt;223&gt; k1aa0427 gene product (K1AA0427) gene.

&lt;400&gt; 67

gtcagatcag ggatcattht ttttccttcc tctactccct cccccctacc cgcctctccc 60  
tccctgtttc ctttccctcc ctccctcccc tctctgtctg gtctgtgctc tggggcgccc 120  
gatccctcc gcagctggga cgctccgaac tcgaggcagg agtcggctct ccggagcctc 180  
gtccctccct tcccttccc tgcccccttc cccaccccc gactcgggct tggcgcgcg 240  
gccagaggaa ccccgagtc cggcccaggc cctgagctg ga gggatgga aaactcctct 300  
gcagcatcag cctcctcgga ggcagggagc agccgctccc aggagatcga ggagctggag 360  
cgcttcacgc acagctacgt gctggagtag caggtgcagg ggctgctggc tgacaagacg 420  
gagggtagtg gcgagagcga gaggacccag tcccacatct cccagtgagc agcggactgc 480  
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ggcagcaaaag acaactctct ggacatgctg ggcacggaca tctgggcggc caacaccttc 600  
gattccttca gtgtgtccac ctgggacctg cagccggaaa agctggactt caccagttc 660  
caccgcaaag tccgacacac gcccaagcag cccctgccac acatcgaccg cgaagggtgt 720  
ggcaaaggga agctggaaga tgggatggc atcaacctga atgacatcga gaaggtcctt 780  
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ctgttccgca ggaggagaaa tgatcgaagg cggcagcaga gacctccggg gggcaacaag 900  
cccaacagc atggtgacca ccagccaggc agtgccaaac acaacaggga ccaccagaaa 960  
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cagaaccggc gctggcacca tggcaacatg aagcaccac caggcgacaa gggggaggca 1080  
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&lt;210&gt; 68

&lt;211&gt; 377

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(377)

<223> 3' terminal sequence. spleen tyrosine kinase  
(SYK) gene.

&lt;400&gt; 68

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aaattcacca caggcca 377
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&lt;210&gt; 69

&lt;211&gt; 323

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(323)

<223> 5' terminal sequence. spleen tyrosine kinase  
(SYK) gene.

&lt;400&gt; 69

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ctgcccagg gaaccgncaa gagagtactg tgtcattcaa tccgtatgag gccaggaact 180
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agaggtgtta cggaggagcc cntacggcgg gaccccgagg gagnttcagg gcccaagggn 300  
gtttttactt gggggaccga aag 323

&lt;210&gt; 70

&lt;211&gt; 2541

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2541)

&lt;223&gt; spleen tyrosine kinase (SYK) gene.

&lt;400&gt; 70

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<210> 71  
<211> 312  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(312)  
<223> 5' terminal sequence. interleukin 7 receptor  
(IL7R) gene.

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<210> 72  
<211> 1658  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(1658)  
<223> interleukin 7 receptor (IL7R) gene.

<400> 72  
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<210> 73  
 <211> 236  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(236)  
 <223> 3' terminal sequence. v-myc avian  
 myelocytomatosis viral oncogene homolog (MYC)  
 gene.

<400> 73  
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<210> 74  
 <211> 413  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(413)  
 <223> 5' terminal sequence. v-myc avian  
 myelocytomatosis viral oncogene homolog (MYC)  
 gene.

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<210> 75  
 <211> 2121  
 <212> DNA/RNA  
 <213> Artificial Sequence

<220>

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&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2121)

<223> v-myc avian myelocytomatosis viral oncogene  
homolog (MYC) gene.

&lt;400&gt; 75

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actcggaagg actatcctgc tgccaagagg gtcaagttgg acagtgtcag agtctgaga 1560
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aagaggcgaa cacacaacgt cttggagcgc cagaggagga acgagctaaa acggagcttt 1680
tttccctgc gtgaccagat ccgggagttg gaaaacaatg aaaaggcccc caaggtagtt 1740
atccttaaaa aagccacagc atacatctg tccgtccaag cagaggagca aaagtcatt 1800
tctgaagagg acttggtgcg gaaacgacga gaacagttga aa cacaact tgaacagcta 1860
cggaactctt gtgcgtaagg aaaagtaagg aaaacgattc cttctaacag aaatgtcctg 1920
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gagtcttgag actgaaagat ttagccataa tgtaaaactgc ctcaaattgg actttgggca 2040
taaaagaact tttttat gct taccatctt ttttttctt taacagattt gtatttaaga 2100
attgttttta aaaaatttta a 2121
```

&lt;210&gt; 76

&lt;211&gt; 260

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(260)

<223> 3' terminal sequence. gata -binding protein 3  
(GATA3) gene.

54/292

&lt;400&gt; 76

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tcacagcact agagaccctg ttaaataggg gatatgagtc agaatggctt attcacagat 60
ggggccaga ttcaagtgggtt ggaacacaga caccacagtg agtcctttg caaagtggca 120
aacataattt tgctttctgc cttcaaaaac atatatccat cgcgtttagg cttcatgata 180
ctgctcctgc aaaaatgcaa gtcgaaaggg actgcaggga ctctcgctgg ggggccctgt 240
gagcatcgag cagggctctt                260
```

&lt;210&gt; 77

&lt;211&gt; 409

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(409)

<223> 5' terminal sequence. gata -binding protein 3  
(GATA3) gene.

&lt;400&gt; 77

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cattctgggt catagatggc atcttttcac tgtgttctca cattgggtga aaggaagaac 60
tctggtttct tcacttcctt ataaggcac caatcttatt cagagggct tcaccctcga 120
aataatcacg tctcaaaaac cccaccttc taatattcta ataccatcac gtgagggctt 180
aggtttcaac ataagaattc ggtggtggtt gggttngggg gagagggaaa caaacatcca 240
gaccagaaac cgaaaaatgt ctacgaaatc caaaaagtgc aaaaaagt gc atgactcact 300
ggaggacttc cccaagganc agctncgttt taacccgggc cgccttttc caggacacat 360
gttccttccc tggnggccac atnttgncc ttnaggccan tccagggca 409
```

&lt;210&gt; 78

&lt;211&gt; 2365

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2365)

&lt;223&gt; gata-binding protein 3 (GATA3) gene.

&lt;400&gt; 78

```
tccagcctt cccatcccc caccgaaagc aaatcattca acgaccccc accctccgac 60
ggcaggagcc ccccgacctc ccaggcggac cgccttccc tccccgcgcg ggttccgggc 120
ccggcgagag ggcgcgacga cagccgaggc catggagggt acggcggacc agccgcgctg 180
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cctcagccac tctacatgg acgcggcgca gtaccgcgtg ccggaggagg tggatgtgct 300
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cacggtgcag aggtaccctc cgaccacca cgggagccag gtgtgccgcc cgcctctgct 420
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gcccgacagc atgaagctgg agtcgtccca ctcccgtggc agcatgaccg ccctgggtgg 78 0
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ctccggactc ttcccccca gcagcctgct ggcgggctcc cccaccggct tcggatgcaa 900
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tattgcatct gggtagctgt aaggcatgaa ggatgccaag aagtttaagg aatatgggag 1860
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ttatacagac cgaactgttg tataaattta tttactgcta gtcttaagaa ctgctttcct 2280
tcgtttgttt gtttcaa tat tttccttctc tctcaatttt cggttgaata aactagatta 2340
cattcagttg gcaaaaaaaaa aaaaa 2365
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<210> 79

<211> 328

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(328)

<223> 3' terminal sequence. growth factor  
receptor-bound protein 7 (GRB7) gene.

<400> 79

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tccctgcctt agagcagcag ctccagagct aggagaagga gagggggcca cccaaggcct 180
tcccttgagg agaggggtca ggagtggact ggagtggggg ctgttttcta tctgaggagg 240
gcaaagaagc agaggagaaa actggagtgg cggaaccctc ccgntcctca tcccgctccc 300
tgtggccgat cccanagtcc actnggat 328
```

<210> 80

<211> 428

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(428)



<223> 5' terminal sequence. growth factor  
receptor-bound protein 7 (GRB7) gene.

<400> 80

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catgctgggc gtgtcattga gaacccccgg gaggtcttga gtgtggccct ggaggaggcc 120
caggcctgga ggaagaagac aaaccaccgc ctacgcctgc ccatgccagc ctccggacga 180
gcctcagtgc agccatccac cgcacccaac tctggttcca cgggcgcatt tcccgtgagg 240
agagccagcg tttattggga cagcagggct tngtagacgg cctgttcttg ggtccgggag 300
agtcagcggg aacccccagg ggtttttcct ctttttnttg ccaccttgca gaaagtgaag 360
cnttattttc attccttgcc gagcgaagga ggaagggccg cttttatttt aagcattggt 42 0
tgattggc                                         428
```

<210> 81

<211> 2205

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(2205)

<223> growth factor receptor-bound protein 7  
(GRB7) gene.

<400> 81

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cacagggctc cccccgcct ctgacttctc tgtccgaagt cgggacaccc tctaccacc 60
tgtagagaag cgggagtggg tctgaaataa aatccaggaa tctggggggt cctagacgga 120
gccagacttc ggaacgggtg tctgtctact cctgtctggg ctctctcagg acaagggca c 180
acaactggtt cegttaagcc cctctctcgc tcagacgcca tggagctgga tctgtctcca 240
cctcatctta gcagctctcc ggaagacctt tggccagccc ctgggacccc tctggggact 300
ccccggcccc ctgatacccc tctgcctgag gaggtaaaga ggtcccagcc tctcctcacc 360
ccaaccacgg gcaggaaact tcgagaggag gagaggc gtg ccacctccct cccctctacc 420
cccaaccctt tccctgagct ctgcagtcct ccctcacaga gcccaattct cggggggccc 480
tccagtgcaa gggggctgct cccccgcgat gccagccgcc cccatgtagt aaaggtgtac 540
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tgtgaaatgc tgggtcagcg agctcacgcc ttgagcgacg agacctgggg gctgggtggag 660
tgccaccccc acctagcact ggagcggggt ttgaggagacc acgagtcctg ggtgggaagt 720
cagggtgcct ggcccgtggg cggagatagc cgcttctgtc tccggaaaaa cttcgccaag 780
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```

ggagcgggag ggttccgcc a ctcagtttt ctctctgct tctttgcctc cctcagatag 1980  
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ccccctctcc ttctcctagc tctggaggtg ctgctctagg gcagggaatt atgggagaag 2100  
tgggggcagc ccaggcggtt tcacgcccc cacttt gtac agaccgagag gccagttgat 2160  
ctgctctggt ttatactagt gacaataaag attattttt gatac 2205

<210> 82

<211> 313

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(313)

<223> 5' terminal sequence. topoisomerase (dna) ii  
beta (180kd) (TOP2B) gene.

<400> 82

gaaatttgac agtaatgaag aagattctgc ttctgttttt tcaccatcat ttggtctgaa 60  
acagacagat aaagttccaa gtaaaacggg agctgctaaa aagggtatgt acttatattt 120  
gattgagtta agcattgg at agagatagtt aatgtaaaag gaaatgtaat ttaatttgaa 180  
actatttgca tttttttatc ataaaacaat taagggaagta taagtgtcta taaggaggac 240  
ctctcgtttt ctagccatct gagggcggtta ataaatttct gtaggactta ntttaaagct 300  
gttgantttt taa 313

<210> 83

<211> 4866

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(4866)

<223> topoisomerase (dna) ii beta (180kd) (TOP2B)  
gene.

<400> 83

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acctgggtga acaatgctgc aaaaaaagaa gagtcagaaa ctgccaacaa aaatgattct 120  
tcaaagaagt tgtctgttga gagagtgtat cagaagaaga cacaacttga acacattctt 180  
cttcgtcctg atacatata tgggtcagtg gagccattga cgcagttcat gtgggtgt at 240  
gatgaagatg taggaatgaa ttgcaggag gttaccttg tgccaggttt atacaagatc 300  
tttgatgaaa ttttggttaa tgctgctgac aataaacaga gggataagaa catgacttgt 360  
attaaagttt ctattgatcc tgaatctaac attataagca tttggaataa tgggaaaggc 420  
attccagtag tagaacacaa ggtagagaaa gtttat gtgc ctgctttaat ttttggacag 480  
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gaatacaaac acagttttta gcagacatgg atgaataata tgatgaagac ttctgaagcc 660  
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ttccctcag acttcctac tgagccacct tctctgccac gaaccggtcg g gctaggaaa 4800  
gaagtaaaat attttacaga gtctgatgaa gaagaagatg atgttgattt tgcaatgttt 4860  
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&lt;210&gt; 84

&lt;211&gt; 311

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(311)

<223> 3' terminal sequence. caspase 4,  
apoptosis-related cysteine protease (CASP4) gene.

&lt;400&gt; 84

cacttttatt gaaatacaaa atgttaaata tgcaagctgt actaatgaag gtgctccttg 60  
aagttgatta aggagggtcg ggctgcttgt ggcttccatt ttcaattgcc aggaaagagg 120  
tagaaatata ttgtcatgga cagtcgttct atgggtgggca tttgagcttt ggcccttgga 180  
gtttcaaatg attgctgtac cttccgaaat acttctcta ggtggcagca ccaagaatat 240  
ttctgggaag catgtgatga gttgtgtgat gaagatagag cccattgtg ctgtctctcc 300  
cagggcacgt t 311

&lt;210&gt; 85

&lt;211&gt; 1291

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1291)

<223> caspase 4, apoptosis-related cysteine  
protease (CASP4) gene.

&lt;400&gt; 85

gctctttcca acgtgtgtaa aaaggacaga ggctgttccc tatggcagaa ggcaaccaca 60  
gaaaaaagcc acttaagggt ttggaatccc tgggcaaaga ttctctcact ggtgttttgg 120  
ataacttggg ggaacaaaat gtactgaact ggaaggaaga ggaaaaaag aa atattacg 180  
atgctaaaac tgaagacaaa gttcgggtca tggcagactc tatgcaagag aagcaacgta 240  
tggcaggaca aatgcttctt caaacctttt ttaacataga ccaaatatcc cccaataaaa 300  
aagctcatcc gaatatggag gctggaccac ctgagtcagg agaatctaca gatgccctca 360  
agctttgtcc tcatgaagaa ttctgagac tatgtaaaga aagagctgaa gagatctatc 420  
caataaagga gagaacaac cgacacgcc tggctctcat catatgcaat acagagtgtg 480  
accatctgcc tccgaggaat ggagctgact ttgacatcac agggatgaag gagctacttg 540  
agggtctgga ctatagtgtg gatgtagaag agaacttgac agccagggat atggagtcag 600  
cgctgagggc atttgctacc agaccagagc acaagtcctc tgacagcaca ttcttggtac 660  
tcatgtctca tggcatcctg gaggaatct gcggaactgt gcatgatgag aaaaaaccag 720  
atgtgtgctt ttatgacacc atcttcaga tattcaacaa cgcgaactgc ctgagcttga 780  
aggacaaacc caaggtcatc attgtccagg cctgcagagg tgcaaaccgt ggggaactgt 840  
gggtcagaga ctctccagca tccttgaag tggcctctc acagtcattc gagaacctgg 900  
aggaagatgc tgtttacaag acccacgtgg agaaggactt cattgcttcc tgctcttcaa 960

60/292

```

cgccacacaa cgtgtcctgg agagacagca caatgggctc tatcttcac acacaactca 1020
tcacatgctt ccagaaatat tcttggtg ct gccacctaga ggaagtattt cggaaggtac 1080
agcaatcatt tgaactcca agggccaaag ctcaaatgcc caccatagaa cgactgtcca 1140
tgacaagata tttctacctc tttcctggca attgaaaatg gaagccacaa gcagcccagc 1200
cctccttaat caacttcaag gagcaccttc attagtacag cttgcatatt taacattttg 1260
tatttcaata aaagtgaaga caaaaaaaaaa a 1291

```

&lt;210&gt; 86

&lt;211&gt; 319

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(319)

<223> 5' terminal sequence. tissue inhibitor of metalloproteinase 2 (TIMP2) gene.

&lt;400&gt; 86

```

tggacctatg ggatgagtgt tttattcatg ctgtttccag gaagggatgt cagagctgga 60
ccagtcgaaa cccttgaggg ctttttttgc agttggccac aggggcgttg gaggcctgct 120
tatgggtcct cgatgtcgag aaactcctgc ttgnggaacn ccgcg ccgcg tnnccacgca 180
caggagcctt cacttctctt gatgcaggcg aagaacttgg cctggnnccc gttnatgttc 240
ttctctgtga cccagtcctt ccagaggcac tcgtccgggg agganatgta gcacgggatc 300
atngggcanc gcgtgatct 319

```

&lt;210&gt; 87

&lt;211&gt; 1075

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1075)

<223> tissue inhibitor of metalloproteinase 2 (TIMP2) gene.

&lt;400&gt; 87

```

cgcagcaaac acatccgtag aaggcagcgc ggccgcga g agccgcagcg ccgctcgccc 60
gccgcccccc accccgcgcg cccgcccggc gaattgcgcc ccgcgcccct cccctcgcg 120
ccccgagaca aagaggagag aaagtttgcg cggccgagcg gggcaggtga ggagggtgag 180
ccgcgcggga ggggcccgcg tcggcccggg ctcagcccc gcccgcgccc ccagcccgcg 240
gccgcgagca gcgcccgg ac cccccagcgg cggcccgcg ccgcccagcc ccccgccccg 300
ccatggggcg cgcgcccgcg accctgcggc tggcgctcgg cctcctgctg ctggcgacgc 360
tgcttcgccc ggccgacgcc tgcagctgct ccccggtgca cccgcaacag gcgttttgca 420
atgcagatgt agtgatcagg gccaaagcgg tcagtgcgaa ggaagtggac tctggaaacg 480
acatttatgg caacctatc aagaggatcc agtatgagat caagcagata aagatgttca 540
aagggcctga gaagatata gagtttatct acacggcccc ctctcggca gtgtgtgggg 600
tctcgtgga cgttgaggga aagaaggaat atctcattgc aggaaaggcc gagggggacg 660
gcaagatgca catcacctc tgtgacttca tcgtgccc tg ggacaccctg agcaccaccc 720
agaagaagag cctgaaccac aggtaccaga tgggctgcga gtgcaagatc acgcgctgcc 780
ccatgatccc gtgtacatc tctccccgg acgagtgcct ctggatggac tgggtcacag 840
agaagaacat caacgggcac caggccaagt tcttcgcctg catcaagaga agtgacggct 900

```

61/292

cctgtgctgtg gtaccgcggc gggcgcccc ccaagcagga gtttctcgac atcgaggacc 960  
cataagcagg cctccaacgc ccctgtggcc aactgcaaaa aaagcctcca agggtttcga 1020  
ctgggtccagc tctgacatcc cttcttgga acagcatgaa taaaacactc atccc 1075

<210> 88  
<211> 225  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(225)  
<223> 3' terminal sequence. d-dopachrome  
tautomerase (DDT) gene.

<400> 88  
ttttttgaat gaggaagctc ttttcattta ttctcanatga ggatgaagaa gaggattatg 60  
tgancacagg aatnttgcat ggggataat ccaaagctgg ttatctccag gncctcantn 120  
tgccaagaga tctctctgga agaagcagcc agttcacaga tgccctggat ccctccgtgc 180  
ccaatcataa aaaagtcatg accgtcccta tnttgccaat ntgcc 225

<210> 89  
<211> 312  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(312)  
<223> 5' terminal sequence. d-dopachrome  
tautomerase (DDT) gene.

<400> 89  
cgttcctgga gctggacacg aatttgcccg ccaaccgagt gcccgcggn tngagaaaac 60  
gactctgcgc cgccgtgcc tccatcctgg gcaaacctgc ggaccgctg aacgtgacgg 120  
tacggccggg cctggccatg gcgctgagcg ggtccaccga gcctgctgc cagtgttcca 180  
tctctccat cggcgtagt gggcaccgag agggacaacc gcagccacag cgcccatctc 240  
ttttgagttt ttccaccaag gagctaagcc cctgccaggg acccgat ant tattccnttt 300  
ttttcccttt gg 312

<210> 90  
<211> 666  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(666)  
<223> d-dopachrome tautomerase (DDT) gene.

<400> 90  
gatcccggtg ccagggaccc tgcccagttc caggcgctgc ctaaccaga aacgactggg 60  
cgccggtcc tggaaaggcc ccagcgacg gacatctgag gagctgtttc cgttcctctg 120  
cccgccatgc cgttcctgga gctggacacg aatttgccc ccaaccgagt gcccgcgagg 180  
ctggagaaac gactctgcgc cgccgctgcc tccatcctgg gcaaacctgc ggaccgctg 240  
aacgtgacgg tacggccggg cctggccatg gcgctgagcg ggtccaccga gccctgcgcg 300  
cagctgtcca tctcctccat cggcgtagtg ggcaccgagg aggacaaccg cagccacagc 360  
gccacttct ttgagtttct caccaaggag ctaccctgg gcc aggaccg gatacttacc 420  
cgctttttcc ccttgagtc ctggcagatt ggcaagatag ggacgggtcat gactttttta 480  
tgattgggca cggaggagtc cagggcattc gtgaactggc tgcttcttcc agagagatct 540  
cttggcagag tgagggcctg gagataacca gctttggatt atcccgcatg caacattcct 600  
gtgatcacat aatcctcttc ttcctctca tatgaaataa atgaagagag ctctctcatt 660  
caaaaa 666

<210> 91  
<211> 443  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(443)  
<223> 3' terminal sequence. prolactin (PRL) gene.

<400> 91  
gantttgatg tctctaagga gtcagttttt attttttaag aggagacctg ttacacccaa 60  
gcatggattc aaaagagata caactaaaag aagcttgcaa tggaacggat cattaaggac 120  
cttctcagaa atagatgaaa tggatgtggg cttagca gtt gttgttggtg atgattcggg 180  
cacttcaggg agcttgagga taattgtcga ttttatgtga atccctgcgt aggcaatggg 240  
agagggttata ataaggcagg aaaggcgag actcttcac agccatctgc aggggatggg 300  
aagtccccga ccagacagg gtagatctca tttcttttg gttttcaggg atgaacctgg 360  
gcttgactat ccagcttcca tgnccctctt ggaagccctt ttggttttgc tccctcaatc 420  
ttctacagct tttgggttag ggt 443

<210> 92  
<211> 243  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(243)  
<223> 5' terminal sequence. prolactin (PRL) gene.

<400> 92  
gaagaatcgg aacatacagg ctttgatata aaaggtttat aaagccaata tctgggaaag 60  
agaaaaccgt gagacttcca gatcttctct ggtgaagtgt gtttcttgca acgatcacga 120  
acatgaacat caaaggatcg ccatgggaaa ggtccctcc tgctgctgct ggtgtttcaa 180  
acctgctcct gtgccagagc gtgggcccc ttggcccatc tgtcccgnc gggcttgccc 240  
gat 243

<210> 93  
<211> 833  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(833)  
<223> prolactin (PRL) gene.

<400> 93  
aaacatgaac atcaaaggat cgccatggaa agggctccctc ctgctgctgc tgggtgtcaaa 60  
cctgctgctg tgccagagcg tggccccctt gcccatctgt cccggcgggg ctgccgatg 12 0  
ccaggtgacc cttcgagacc tgtttgaccg cgccgctcgtc ctgtccact acatccataa 180  
cctctctca gaaatgttca gcgaattcga taaacgggtat acccatggcc gggggttcat 240  
taccaaggcc atcaacagct gccacacttc ttcccttgcc accccgaag acaaggagca 300  
agcccaacag atgaatcaaa aagactttct gaggctgata gtcagcatat tgcgacctg 360  
gaatgagcct ctgtatcatc tggtcacgga agtacgtggt atgcaagaag ccccgaggc 420  
tactctatcc aaagctgtag agattgagga gcaaaccaaa cggttcttag agggcatgga 480  
gctgatagtc agccagggtc atcctgaaac caaagaaaat gagatctacc ctgtctggc 540  
gggacttcca tccctgcag a tggctgatga agagtctcgc ctttctgctt attataacct 600  
gctccactgc ctacgcaggg attcacataa aatcgacaat tatctcaagc tctgaagtg 660  
ccgaatcatc cacaacaaca actgctaagc ccacatccat ttcattctatt tctgagaagg 720  
tccttaatga tccgttccat tgcaagcttc ttttagttgt atctcttttg aatccatgct 780  
tgggtgtaac aggtctcctc ttaaaaaata aaaactgact cgttagagac atc 833

<210> 94  
<211> 304  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(304)  
<223> 3' terminal sequence. prolactin receptor  
(PRLR) gene.

<400> 94  
actaagcagt gtgcttttat ttcatgtaac acatagtttt ataactaaca gcaaaaagta 60  
aatctacaaa tcacagttag gaaacataat gatttgttct ggaatcagct gctggagaaa 120  
gaggcaagtg gttaaaaatg gagcatgaaa ggagctggga gcttttagtag tgtcagtctg 180  
actacattct tgaggcattt cagctactct gtagtggtac ctgaagaaaa atcacatttt 240  
aaccaatcat tccattagtc aagctatcag tgaaaggagt gtgtaaaaca tgcgggatcc 300  
cggg 304

<210> 95  
<211> 366  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer



&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(366)

<223> 5' terminal sequence. prolactin receptor  
(PRLR) gene.

&lt;400&gt; 95

```
gaggtcattg agaagccaga gaatcctgaa acanccacaca cctggaaccc ccantgcata 60
agcatggaag gcaaaatccc ctatttncat gctggtggat ccaaattgtc aacatggccc 120
ttaccacagc ccagccagca caacccacaga tcctcttacc acaatattac tgatgtgtgt 180
gagctggctg tgggccctgc aggtgcaccg gccactctgt tgaatgaagc aggtaaagat 240
gctttaaaat cctctcaaac cattaagtct agagangag g gnaaggcaac ccaggcagag 300
ggaggtagga aagcttccat tcttgagnac tgaccagggt tacgncctgg gttgcttgcc 360
ccaggg
```

&lt;210&gt; 96

&lt;211&gt; 2723

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2723)

&lt;223&gt; prolactin receptor (PRLR) gene.

&lt;400&gt; 96

```
ggaggctgaa atccccagac gccggttttc tgggctgggc tttctgetta ctcaactcctt 60
ctccctcttt ctggatttta ccgaccgttc gcgaaacagc tttccacaca atggagcttc 120
atgtcctcgt gcaggaagta ctcacgcact gatgtggcag actttgctcc ctgacaaaaa 180
taaagaactc tcctattcat ggaggcgaac actgaggatg ctttccacat gaaccctgaa 240
gtgaacttct gatacatttc ctgcagcaag agaaggcagc caacatgaag gaaaatgtgg 300
catctgcaac cgttttact ctgctacttt ttctcaac ac ctgccttctg aatggacagt 360
tacctcctgg aaaacctgag atctttaaat gtcgttctcc caataaggaa acattcacct 420
gctggtggag gcctgggaca gatggaggac ttctaccaa ttattcactg acttaccaca 480
gggaaggaga gacactcatg catgaatgtc cagactacat aaccgggtgc cccaactcct 540
gccactttgg caagcagtac acctccatgt ggaggacata catcatgatg gtcaatgcca 600
ctaaccagat gggaagcagt ttctcggatg aactttatgt ggacgtgact tacatagttc 660
agccagaccc tcctttggag ctggctgtgg aagtaaaaca gccagaagac agaaaaccct 720
acctgtggat taaatggtct ccacctaccc tgattgactt aaaaactggt tggttcac gc 780
tcctgtatga aattcgatta aaacccgaga aagcagctga gtgggagatc cattttgctg 840
ggcagcaaac agagtttaag attctcagcc tacatccagg acagaaatac cttgtccagg 900
ttcgtgcaa accagaccat ggatactgga gtgcattggag tccagcgacc ttcattcaga 960
tacctagtga cttcaccatg aatgatacaa ccgtgt ggat ctctgtggct gtcccttctg 1020
ctgtcatctg tttgattatt gtctgggcag tggctttgaa gggtatagc atggtgacct 1080
gcatctttcc gccagttcct gggccaaaaa taaaaggatt tgatgctcat ctggttgaga 1140
agggcaagtc tgaagaacta ctgagtgcct tgggatgcca agactttcct ccacttctg 1200
actatgagga cttgctggtg gagtatttag aagtagatga tagtgaggac cagcatctaa 1260
tgtcagtcga ttcaaaagaa cacccaagtc aaggtatgaa acccacatac ctggatcctg 1320
acactgactc aggcggggg agctgtgaca gcccttcctt tttgtctgaa aagtgtgagg 1380
aaccacagc caatccctoc acattctatg atcctgaggt cattgagaag ccagagaatc 1440
ctgaaacaac ccacacctgg gacccocagt gcataagcat ggaaggcaaa atcccctatt 1500
ttcatgctgg tggatccaaa tgttcaacat ggcccttacc acagcccagc cagcacaacc 1560
ccagatcctc ttaccacaat attactgatg tgtgtgagct ggctgtgggc cctgcaggty 1620
caccggccac tctgttgaat gaag caggta aagatgcttt aaaatcctct caaaccatta 1680
agtctagaga agagggaaag gcaaccagc agaggagggt agaaagcttc cattctgaga 1740
ctgaccagga tacgcctggt ctgctgcccc aggagaaaac cccctttggc tccgctaacc 1800
ccttggaatta tgtggaagatt cacaaggatc acaaagatgg tgcattatca ttgctaccaa 1860
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65/292

```
aacagagaga gaacagcggc aagcccaaga agccccggac tcctgagaac aataaggagt 1920
atgccaaagt gtccgggggtc atggataaca acatcctggt gttgggtgcc gatccacatg 1980
ctaaaaacgt ggcttgcttt gaagaatcag ccaaaggagg cccaccatca ctggaacaga 2040
atcaagctga gaaagccctg gccaaactca ctgcaaca tc aagcaagtgc aggctccagc 2100
tggttggttt ggattacctg gatcccgcat gttttacaca ctcttttcac tgatagcttg 2160
actaatggaa tgattggta aaatgtgatt tttcttcagg taacactaca gagtacgtga 2220
aatgctcaag aatgtagtca gactgacact actaaagctc ccagctcctt tcatgctcca 2280
tttttaacca ct tgcctctt tctccagcag ctgattccag aacaaatcat tatgtttcct 2340
aactgtgatt ttagatttta ctttttgctg ttagttataa aactatgtgt tcaatgaaat 2400
aaaagcacac tgcttagtat tcttgaggga caatgccaat aggtatatcc tctggaaaag 2460
gctttcatga tttggcatgg gacagacgga aatgaaattg tcaaaattgt t taccataga 2520
aagatgacaa aagaaaattt tccacatagg aaaatgccat gaaaattgct ttgaaaaaac 2580
aactgcataa cctttacact cctcgtccat tttattagga ttacccaaat ataaccattt 2640
aaagaaagaa tgcattccag aacaaattgt ttacataagt tcctatacct tactgacaca 2700
ttgctgatat gcaagtaaga aat                                     2723
```

&lt;210&gt; 97

&lt;211&gt; 365

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(365)

<223> 3' terminal sequence. interleukin 2  
receptor, beta (IL2RB) gene.

&lt;400&gt; 97

```
gtacagttac cttttattta tagcgaaaat gggttttttc atttacagag taacaaagat 60
ttttctttta ataaatgtat ttcaacgaaa atgaactgac ttaaagaaaa aatattaagg 120
aaataatcac aaagatggta cacacggatc attaaaagat acggatgtat aggatacata 180
tgtcacaaat gattaaggac ttaaaaaatg taaccctccc aagaagtggg gagcctccca 240
aagtggggga agggcaaata caatttccnt ttgggggggg atagggngac cccctttgca 300
gagagggggt aggtgggggt tcccccggn acacacaggc aagggttttg gngccccttg 360
tgggg                                           365
```

&lt;210&gt; 98

&lt;211&gt; 366

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(366)

<223> 5' terminal sequence. interleukin 2  
receptor, beta (IL2RB) gene.

&lt;400&gt; 98

```
nattcggcac tagggggcac ctgaccacac gccccacag gctctgacca gcagcctatg 60
agggggtttg gcaccaagct ctgtccaatc aggtaggctg ggctgaacta gccaatcaga 120
tcaactctgt cttgggcgtt tgaactcagg gagggaggcc cttgggagca ggtgcttggt 180
gacaaggctc cacaagcgtt gagccttgga aaggtagaca agcgttg agc cactaagcag 240
aggaccttgg gttccaata caaaaatacc tactgctgag aggggntgct gaccattttg 300
```

gtcaaggatt tcngtttgcc ttatatccca aataaantcc ctttttttn aggtttntt 360  
agtntt 366

<210> 99

<211> 4034

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(4034)

<223> interleukin 2 receptor, beta (IL2RB) gene.

<400> 99

gcagccagag ctcagcaggg ccctggagag atggccacgg tcccagcacc ggggagg act 60  
ggagagcgcg cgctgccacc gcccattgtc tcagccaggg cttccttcct cggctccacc 120  
ctgtggatgt aatggcgggc cctgctctgt cctggcgtct gcccctctc atcctcctcc 180  
tgccccctggc tacctcttgg gcatctgcag cggatgaatgg cacttcccag ttcacatgct 240  
tctacaactc gagagccaac atctcctgtg tctgga gcc aagatggggct ctgcaggaca 300  
cttcctgcca agtccatgcc tggccggaca gacggcggtg gaaccaaacc tgtgagctgc 360  
tccccgtgag tcaagcatcc tgggcctgca acctgatcct cggagcccca gattctcaga 420  
aactgaccac agttgacatc gtcaccctga ggggtgctgtg ccgtgagggg gtgcgatgga 480  
gggtgatggc catcaggac ttcaagccct ttgagaacct tcgctgatg gcccctatct 540  
ccctccaagt tgtccacgtg gagaccaca gatgcaacat aagctgggaa atctcccaag 600  
cctcccaacta ctttgaaga cacctggagt tcgaggcccg gacgtgttcc ccaggccaca 660  
cctgggagga ggccccctg ctgactctca agcagaagca ggaatggatc tgcctg gaga 720  
cgctcaccac agacaccag tatgagtttc aggtgcggt caagcctctg caaggcgagt 780  
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ttccttaata ttttttcttt aagtcagttc attttcgttg aaatacattt ataaagaaaa 3960
atctttgtta ctctgtaaat gaaaaaacc attttcgcta taaataaaag gtaactgtac 4020
aaaataagta caat 4034
```

<210> 100

<211> 444

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(444)

<223> 3' terminal sequence. gata -binding protein 3  
(GATA3) gene.

<400> 100

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tttctatttt tttattttct tttaatgcat caaacaactg tggccagtga aaggaaacaa 60
aactggcagt ttgtccattt gaatatcaga cctagtttct tcttaatttc cacacta ttt 120
ctcccatatt ccttaaaactt cttggcatcc ttcattgcctt acagctaccc agatgcaata 180
aagtcattgt acagtatttc ttacaatata agttatatgg caatgttcag gcattttttt 240
ttttcacagg cactaggagg accctgttta aatgggggat atgaggtcag gaatgggctt 300
attcacagga tgggggggtcc cggattcagg tgggt tgggg ancacaggac accacagggtg 360
aggctccctt tgccaaagggt ggggccaaac ataatttttg cttttctggc ccttcaaaaa 420
catatttccn tcgcgttttg gggg 444
```

<210> 101

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

68/292

<221> misc\_feature  
<222> (1)..(396)  
<223> 5' terminal sequence. gata-binding protein 3  
(GATA3) gene.

<400> 101  
gcaatgggga ccctgtctgc aatgcctgtg gntctactac aagcttcaca atattaacag 60  
acccttgact atgaagaagg aaggcatcc a gaccagaaac cgaaaaatgt ctacaaatc 120  
caaaaagtgc aaaaagtgc tgactcactg gaggacttcc ccaagaacag ctggtttaac 180  
ccggccgccc tctccagaca catgtcctcc ctgagccaca tctcgccctt cagccactcc 240  
agccacatgc tgaccacggc ccacgccgat ggcacccgcc atccagcctg tcctttggga 300  
ccacaccacc cctccagctg ggtcacccgcc ntgggttttag agccttgtn gatggttcac 360  
agggggcccc cagcgagagt tncctgnagt tccttt 396

<210> 102  
<211> 416  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(416)  
<223> 5' terminal sequence. placental growth  
factor, vascular endothelial growth factor -related  
protein (PGF) gene.

<400> 102  
attcggcact aggggagacc caagggcagg gggaagagga ggagagagaa gcagagaccc 60  
acagactgcc acctgtgcgg cgatgctgtt ccccgagta acccaccctt tggaggagag 120  
agaccccgca cccggctcgt gtatttatta ccgtcacact cttcagtgc tctgctggt 180  
acctgccctc tatttattag ccaactgttt cctgctgaa tgcctcgctc cttcaagac 240  
gaggggcagg gaaggacagg accctcagga attcagtgc ttcaacaacg tga gagaaag 300  
agagaagcca gccacagacc cctggggagc tttccgcttt tgaaagaagc aagacaagt 360  
ggccttggtg aggggcaagg ttagggccca ggagccctn gggaagtttt tcaggg 416

<210> 103  
<211> 1645  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(1645)  
<223> placental growth factor, vascular  
endothelial growth factor-related protein (PGF)  
gene.

<400> 103  
gggattcggg ccgcccagct acgggaggac ctggagtggc actgggcgcc cgacggacca 60  
tccccgggac ccgctgccc ctggcgccc cgccccgcc ggccgctccc cgtcgggttc 120  
cccagccaca gccttaccta cgggctcctg actccgcaag gcttcagaa gatgctcga 180  
ccaccggccg gggcctcggg gcagcagtga gggaggcgtc cagccccca ctcagctctt 240  
ctctcctgt gccaggggct ccccggggga tgagcatggt ggttttcctt cgagacccc 300

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tggctcggga cgtctgagaa gatgccggtc atgaggctgt tcccttgctt cctgcagctc 360
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ggctcgtcag aggtggaagt ggtacccttc caggaagtgt ggggccgcag ctactgcccg 480
gcgctggaga ggctggtgga cgtcgtgtc c gagtacccca gcgaggtgga gcacatgttc 540
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gcagaaggaa agaagggggc cctgctacct gttcttgggc ctcaggctct gcacagacaa 1140
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ataaagtatt ctagtgtgga aacgc 1645

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<210> 104  
 <211> 309  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(309)  
 <223> 5' terminal sequence. ubiquitin protein  
 ligase e3a (human papilloma virus e6 -associated  
 protein, angelman syndrome) (UBE3A) gene.

```

<400> 104
ttcggcanag gggaaatgaa gcctgcacga atgagttttg tgcttcctgt ccaacttttc 60
ttcgtatgga taataatgca gcagctatta aagccctcga gctttataag antagggcaa 120
aactctgtga tcctcatccc tccaagaaag gagcaagctc agcttacctt gagaactcga 180
aaggtgcccc caacaactcc tgctctgaga taaaaatgaa caaggaaagg gcgctaggaa 240
ttggatttta aagatgtgac ttactttaac aggaaggagg aagggtatta tggaaaattt 300
tctttggac 309

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<210> 105  
 <211> 2628  
 <212> DNA/RNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(2628)  
 <223> ubiquitin protein ligase e3a (human

papilloma virus e6-associated protein, angelman  
syndrome) (UBE3A) gene.

<400> 105

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gctagccgaa tgaagcgagc agctgcaaag catctaatag aacgctacta ccaccagtta 120
actgaggcct gtggaaatga agcctgcacg aatgagtttt gtgcttcctg tccaactttt 180
cttcgtatgg ataataatgc agcagctatt aaagccctcg agctttataa gattaatgca 240
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aaaggtgccc ccaacaactc ctgctctgag ataaaaatga aca agaaagg cgctagaatt 360
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gaggcattgg tactagagctt ccggaagtt aaacaacaca ccaaggaaga actgaaatct 540
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gctgctatgg aagaagactc agaagcatct tcctcaagga taggtgatag ctcacaggga 660
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ggaaaattaa agatgattat agccaaaaat ggcccagaca cagaaaggtt acctaca tct 2520
catacttgct ttaatgtgct tttacttccg gaataactca gcaaagaaaa acttaaaagag 2580
agattgttga aggccatcac gtatgccaaa ggatttggca tgctgtaa 2628
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<210> 106

<211> 363

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence :primer

<220>

<221> misc\_feature

<222> (1)..(363)

<223> 3' terminal sequence. oncogene tc21 (TC21)  
gene.

<400> 106

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aattttaatt ctagcacctg aagctataca agggatatgct ctataaactt catgggactg 60
tcgtacacac ttgataaagt gacaactgtg caataccact tagcatctca aaatcag gaa 120
catactattg aattgcttaa acacaatcca caganttaaa aacaaaatca ggatgccatc 180
cacagtata ctaattatcc attaaaaggc ttacacttaa tacttgaant aacaatcaat 240
atctagncgg ggnatactgg aaagtggatt tcagnggtct catcctgttg gtactctatt 300
ggggnggggt ttcttgaggt aggttatggt ggact gggnc caaggntggg ggggtaccacc 360
cag 363
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<210> 107

<211> 408

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(408)

<223> 5' terminal sequence. oncogene tc21 (TC21)  
gene.

<400> 107

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gaattgaatc taaaaaagtg aaccatctca gacctttact gatactacaa cttttgtttt 60
ctgatggcca aaataccaaa tgctgttgtt atttatggat taaaaactgc ttataaaacc 120
ctgtgttact actcctactc ttggagatga taatatct ta tgtgggtcaaa tatttggact 180
catttaggac ttagatattt cagtgtactt gatTTTTTaa ttttaactctt tttcacagcc 240
acgctaaggg taaaaaggaa taatttcctt ctgtcttcct tttcaagtat ttctgggtaa 300
gggattcaaa aaactaaaac tgTTTTgtt tgtaatatata aatatgggat tgatctttcc 360
ggggtcagag atgattaatg tttttgctat atacttttat acatgnnt 408
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<210> 108

<211> 612

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(612)

<223> oncogene tc21 (TC21) gene.

<400> 108

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gggggcggcg tgggcaagtc ggcgctcacc atccagttca tccagtccta ttttctaacc 120
gattatgac caaccattga agattcttac acaaagcagt gtgtgataga tgacagagca 180
gcccgctag atattttgga tacagcagga caagaagagt t tggagccat gagagaacag 240
tatatgagga ctggcgaagg cttcctgttg gtcttttcag tcacagatag aggcagtttt 300
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ggacaacagt tagcacggca gcttaaggta acatacatgg aggcacagc aaagattagg 480
atgaatgtag atcaagcttt ccatgaactt gtccgggtta tcaggaaatt tcaagagcag 540
gaatgtcctc cttcaccaga accaacacgg aaagaaaaag acaagaaagg ctgccattgt 600
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gtcattttct ag

6 12

<210> 109  
<211> 592  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(592)  
<223> 5' terminal sequence. tyrosine kinase with  
immunoglobulin and epidermal growth facto r  
homology domains (TIE) gene.

<400> 109  
ngtcggagag aacctagcct ccaagattgc agacttcggc ctttctcggg gagaggaggt 60  
ttatgtgaag aagacgatgg ggcgtctccc tgtgcgctgg atggccattg agtccctgaa 120  
ctacagtgtc tataccacca agagtgatgt ctggtccttt ggagtccttc tttgggagat 1 80  
agtgagcctt ggaggtacac cctactgtgg catgacctgt gccgagctct atgaaaagct 240  
gccccagggc taccgcatgg agcagcctcg aaactgtgac gatgaagtgt acgagctgat 300  
gcgttcagt ctggcgggac cgtccctatg agcgaccccc ctttgcccag attgcgctaa 360  
cagctaggcc gcatgctggg aagccaggga aggcctatgt gaacatgttc gctgtttgag 420  
aacttcaatt aacgcgggca ttgatgccac agctgaggag gnetgagctg ccaccagcc 480  
agaactnggt ctgttgccg gagcaaattt ggtgtctaaa ctgtgaccag ttnaacctta 540  
aagctttgat ttaagttgct taaggatttt ttaattaag ggagaaaaat tt 592

<210> 110  
<211> 3845  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(3845)  
<223> tyrosine kinase with immunoglobulin and  
epidermal growth factor homology domains (TIE)  
gene.

<400> 110  
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<210> 111

<211> 202

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(202)  
<223> 3' terminal sequence. autocrine motility  
factor receptor (AMFR) gene.

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<210> 112  
<211> 450  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(450)  
<223> 5' terminal sequence. autocrine motility  
factor receptor (AMFR) gene.

<400> 112  
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<210> 113  
<211> 1810  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(1810)  
<223> autocrine motility factor receptor (AMFR)  
gene.

<400> 113  
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<210> 114

<211> 248

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(248)

<223> 3' terminal sequence. homo sapiens mrna;  
cdna dkfzp434c136 (from clone dkfzp434c136) (EST  
R81127) gene.

<400> 114

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<210> 115

<211> 415

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(415)

<223> 3' terminal sequence. b-cell cll/lymphoma 2  
(BCL2) gene.

<400> 115  
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gtttcanggc tgattctaaa ctggangaaa aaaaaaattn cctagtttat ttgctganga 180  
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ggggtgtaca ggataacccc catattccac accggggnac ttttttttg tcagggtttt 300  
caaataaaanc caaactacag tgacaggata atgttttaca ggtaattccn tgggccgggg 360  
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<210> 116

<211> 468

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(468)

<223> 5' terminal sequence. b-cell cll/lymphoma 2  
(BCL2) gene.

<400> 116  
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gagtaagaaa cagaatcctc tggaacttga ggaagtgaac atttcggtga cttccgcac 180  
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<210> 117

<211> 6030

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(6030)

<223> b-cell cll/lymphoma 2 (BCL2) gene.

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gagcacagaa gatgggaaca ctggtgga gg atggaaaggc tcgctcaatc aagaaaattc 5460
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tggtgttga aaaagtcaca ttgccattaa actttccttg tctgtctagt taatattgtg 6000
aagaaaaata aagtacagtg tgagatactg 6030

```

&lt;210&gt; 118

&lt;211&gt; 343

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(343)

<223> 5' terminal sequence. v-erb-b2 avian  
erythroblastic leukemia viral oncogene homolog 2  
(neuro/glioblastoma derived oncogene homolog)  
(ERBB2) gene.

&lt;400&gt; 118

```

caagggggtg caaactnncc cacacatgac ccagccctc tacagcggta cagtgaggac 60
cccacagtac cctgcctc tgagactgat ggctacgttg ccccttgac ctgcagcccc 120
cagcctgaat atgtgaacca gccagatgtt cggccccagc cccct tcgcc ccgagaggcc 180
ctctgcctgc tgcccacact gctggtgcca ctctggaaag gcccaagact ctctcccag 240
ggaagaatgg ggtcgtcaaa gagtttttgc ctttgggggt gccgtgggag aaccccagat 300
attgacaccc caggggaggg agcttgccct tcagccccac ctt 343

```

&lt;210&gt; 119

&lt;211&gt; 4530

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(4530)

<223> v-erb-b2 avian erythroblastic leukemia viral  
oncogene homolog 2 (neuro/glioblastoma derived  
oncogene homolog) (ERBB2) gene.

&lt;400&gt; 119

```
aattctcgag ctgctcgacc ggtcgacgag ctcgagggtc gacgagctcg agggcgcgcg 60
ccccgcccc accctcgca gcaccccgcg ccccgcgccc tcccagccgg gtccagccgg 120
agccatgggg ccggagccgc agtgagcacc atggagctgg cggccttggt ccgctggggg 180
ctcctcctcg ccctcttgcc ccccgagacc gcgagcacc aagtgtgcac cggcacagac 240
atgaagctgc ggctccctgc cagtcccgag acccacctgg acatgctccg ccacctctac 300
cagggctgcc aggtggtgca gggaaacctg gaactcacct acctgccac caatgccagc 360
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```



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aatgaggact tggggccagc cagtcccttg gacagcacct tctaccgctc actgctggag 3180
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ccctttcctt ccagatcctg ggtactgaaa gccttaggga agctggcctg agaggggaag 4260
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ttgtccattt gcaaatatat tttgaaaa c 4530

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&lt;210&gt; 120

&lt;211&gt; 319

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(319)

<223> 5' terminal sequence. mouse double minute 2,  
human homolog of; p53-binding protein (MDM2) gene.

&lt;400&gt; 120

```

nacttatttc ccctagtga cctgtctata agagaattat atatttctaa ctatataacc 60
ctaggaattt agacaacctg aaatttatc acatatatca aagtgagaaa atgcctcaat 120
tcacatagat ttcttctctt tagtataatt gacctacttt ggtagtggga a tagtgaata 180
cttactataa ttgacttga atatgtaggc tcacccctta caccaactcc taattttaaa 240
taatttttac tctgtcttaa atgaggagg acttgggntt ttttttttct taaatatggt 300
atatggacat ttaaatggt 319

```

&lt;210&gt; 121

&lt;211&gt; 2372

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

<222> (1)..(2372)

<223> mouse double minute 2, human homolog of;  
p53-binding protein (MDM2) gene.

<400> 121

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gcaccgcgcg agcttggtcg cttct ggggc ctgtgtggcc ctgtgtgtcg gaaagatgga 60
gcaagaagcc gagcccgagg ggcgcccgcg acccctctga ccgagatcct gctgctttcg 120
cagccaggag caccgtccct ccccgatta gtgcgtacga gcgcccagtg ccctggccccg 180
gagagtggaa tgatccccga ggcccagggc gtcgtgcttc cgcagtagtc agtccccgtg 240
aaggaaactg gggagtcttg agggaccccc gactccaagc gcgaaaaccc cggatggtga 300
ggagcaggca aatgtgcaat accaacaatgt ctgtacctac tgatggtgct gtaaccacct 360
cacagattcc agcttcggaa caagagaccc tggtttagacc aaagccattg cttttgaagt 420
tattaaagtc tgttggtgca caaaaagaca cttatactat gaaaga ggtt cttttttatc 480
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gttcaaata tcttctagga gatttgtttg gcgtgccaaag cttctctgtg aaagagcaca 600
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aagaaaccca agacaaagaa gagagtgtgg aatctagttt gcccttaat gccattgaac 1620
cttgtgtgat ttgtcaaggt cgacctaaaa atggttgcat tgtccatggc aaaacaggac 1680
atcttatggc ctgctttaca tgtgcaaaga agctaaagaa aaggaataag ccctgccag 1740
tatgtagaca accaattcaa actatataac ctaggaatt tagacaacct gaaatttatt 1800
aagagaatta tatatttcta actatataac ctaggaatt tagacaacct gaaatttatt 1860
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tacagtcata tgccaccaca cctggcta at tttttgtact tttagtagag acagggtttc 2280
accgtgttag ccaggatggt ctgatctcc tgacctctg atccgccac ctggcctcc 2340
caaagtgcgt ggattacagg catgagccac cg 2372
```

<210> 122

<211> 343

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(343)

<223> 3' terminal sequence. gata-binding protein 3  
(GATA3) gene.

<400> 122  
atgcttataa tattattcca acagactgta tta aaggcag tgatcactaa cacagancac 60  
gacagggcga ngaggcagcc nggcccataa ncaggacgtg gccnntcggc cagggttcgc 120  
tgacatgcac gctggtagct catacactgc taccctcagc acaggctgca ggaataggga 180  
caagacagat gccgccggac tcttaggaag ctatttaata aatatcatcc aaanacaaaa 240  
tgggaaaagg aaacaaggaa accctccggg gcacaaccac cttaggggcc aactggaatg 300  
gtaattctag gttttatttc caacccaaaa nttgaggaga gga 343

<210> 123  
<211> 258  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(258)  
<223> 3' terminal sequence. src homology 3  
domain-containing protein hip-55 (HIP-55) gene.

<400> 123  
cgagttagnt atgttgagg aacatgttgt gtctgccgtt tttgaatacc cagggtggga 60  
gcttgccat ctgcatcccc acttoccata gcccaggcag agggac agag aaatggagtn 120  
gggagcacag agcaggtcc aacaagacaa attccctgct gccaaaccac catgatccac 180  
tctgactttg gncacaaact ctgctaaaaa caattctcta cgttcactgt tccaagggg 240  
canttttaaa cagtgggtg 258

<210> 124  
<211> 443  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(443)  
<223> 5' terminal sequence. src homology 3  
domain-containing protein hip-55 (HIP-55) gene.

<400> 124  
gccagggtc agtgggcaag ggctctgtgc cgtngnccgtg tacgactacc atgcagccga 60  
cgacacagag atctcctttg accccgagaa cctcatcacg ggcacgagg tgatcgacga 120  
aggctgtgg cgtggtatg gcccgatca tntgttngca tgttccctgc caactacgtg 180  
gagctcattg agtgaggctg agggcacatc ttgcccttcc cctctcagac atggcttc ct 240  
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ccccagttga ggattgaggc ntcagggttc cctccggnnt gggcagattc agccttttca 360  
ccccaaatgg cagcaattgg cntgggtgat ttcccacaaa tcnttctctg cattcccccg 420  
acctttccca gacagtttg ttt 443

<210> 125  
<211> 1331  
<212> DNA/RNA  
<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1331)

<223> src homology 3 domain-containing protein  
hip-55 (HIP-55) gene.

&lt;400&gt; 125

```
atggcggcga acctgagccg gaacggggcca gcgctgcaag aggcctacgt gcgggtgggtc 60
accgagaagt ccccgaccga ctgggctctc ttacctatg aaggcaacag caatgacatc 120
cgctggctg gcacagggga ggggtggcctg gaggagatgg tggaggagct caacagcggg 180
aagtgatgt acgccttctg cagagtgaag gacccaact ctggactgcc caaatttgtc 240
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agagaaaaaa c 1331
```

&lt;210&gt; 126

&lt;211&gt; 430

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(430)

<223> 3' terminal sequence. cathepsin d (lysosomal  
aspartyl protease) (CTSD) gene.

&lt;400&gt; 126

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gtatttccat gtcagctggg gctctcagcc gcccaagggg aggacaacag aggtcagctg 60
cagaggaagg ctggcaccag ccccaatccc aacccacact ccaggccaat acatgcccct 120
gggactggct cagtcccagc accaccctgc aggtccaac aaggtgggtt ttgtcccctc 180
tactccttc cagtcaccc tcaggcctct agcggcctca tcctcaacgg gcccgggaca 240
ctgaacaggt aggtgggca gagccagctg ggncccaagc tnggcaagag gggccctcag 300
gcaggcgagg ttttncagg gaggncccg gaggacggc ttgggtnttg g ggtaagggc 360
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aanccccagg 430
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&lt;210&gt; 127

<211> 339  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(339)  
<223> 5' terminal sequence. cathepsin d (lysosomal  
aspartyl protease) (CTSD) gene.

<400> 127  
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acatgatccc ctgtgagaag gtgtccacc c tggccgcat cacactgaag ctgggaggca 120  
aaggctacaa gctgtcccca gaggactaca cgtcaaggt gtcgcaggcc gggaagaccc 180  
tctgctgag cggcttcatt ggcatggaca tcccgccacc cagcggnac tctggatcct 240  
ggggcgacgt cttcattcgg ccgttantac attgtgtttt gaccgtgaca acaacagggg 300  
tgggtttcgc gaggcttgcc cgcttttagt ttcccaagg 339

<210> 128  
<211> 1988  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(1988)  
<223> cathepsin d (lysosomal aspartyl protease)  
(CTSD) gene.

<400> 128  
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ctcccctc 1988

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&lt;210&gt; 129

&lt;211&gt; 385

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(385)

&lt;223&gt; 5' terminal sequence. insulin-like growth factor 1 receptor (IGF1R) gene.

&lt;400&gt; 129

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&lt;210&gt; 130

&lt;211&gt; 4989

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(4989)

&lt;223&gt; insulin-like growth factor 1 receptor (IGF1R) gene.

&lt;400&gt; 130

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&lt;210&gt; 131

&lt;211&gt; 470

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(470)

<223> 5' terminal sequence. insulin receptor  
(INSR) gene.

&lt;400&gt; 131

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&lt;210&gt; 132

&lt;211&gt; 4691

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(4691)

&lt;223&gt; insulin receptor (INSR) gene.

&lt;400&gt; 132

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ggtgtctgag cttcagtata aaagacaaa ctctctgtt gtggaacaaa atttcgaaag 4680
aaaaaaccaa a
4691

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&lt;210&gt; 133

&lt;211&gt; 451

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(451)

<223> 5' terminal sequence. forkhead box ola  
(rhabdomyosarcoma) (FOXO1A) gene.

&lt;400&gt; 133

```

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tcccaagttg attttggatg gcttttttt t
451

```

&lt;210&gt; 134

&lt;211&gt; 5723

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(5723)

<223> forkhead box ola (rhabdomyosarcoma) (FOXO1A)  
gene.

&lt;400&gt; 134

```

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&lt;210&gt; 135

&lt;211&gt; 466

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(466)

<223> 3' terminal sequence. epidermal growth  
factor receptor (avian erythroblasti c leukemia  
viral (v-erb-b) oncogene homolog) (EGFR) gene.

&lt;400&gt; 135

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&lt;210&gt; 136

&lt;211&gt; 450

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(450)

<223> 5' terminal sequence. epidermal growth  
factor receptor (avian erythroblastic leukemia  
viral (v-erb-b) oncogene homolog) (EGFR) gene.

<400> 136

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<210> 137

<211> 5532

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(5532)

<223> epidermal growth factor receptor (avian  
erythroblastic leukemia viral (v-erb-b) oncogene  
homolog) (EGFR) gene.

<400> 137

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94/292

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agatgtttta gaaggaaaaa agtt ccttcc taaaataatt tctctacaat tggaagattg 5220
gaagattcag ctagttagga gccattttt tcctaactctg tgtgtgccct gtaacctgac 5280
tggttaacag cagtcctttg taaacagtgt tttaaactct cctagtcaat atccaccca 5340
tccaatttat caaggaagaa atggttcaga aaatattttc agcctacagt tatgttcagt 540 0
cacacacaca taaaaaatgt tccttttgct tttaaagtaa tttttgactc ccagatcagt 5460
cagagcccct acagcattgt taagaaagta ttgattttt gtctcaatga aaataaaact 5520
atattcattt cc 5532

```

&lt;210&gt; 138

&lt;211&gt; 378

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(378)

<223> 3' terminal sequence. tek tyrosine kinase,  
endothelial (venous malformations, multiple  
cutaneous and mucosal) (TEK) gene.

&lt;400&gt; 138

```

ggatnagant ttanaggcaa gacatttatt cactcatgat atatcagtgc aaagtgtgcc 60
tacagtatac aaggtaaact cacaactcat caaaactaaa actttttaca atgtgcaata 120
catgtaggga tattaattca atatataaat gtcacatgtc tcccaaagt caccaggct 180
ttctgttatt tcttaaaata tacaagtcaa t attaccaga gaaaagataa gaaaatccca 240
ttattttatc ctaaaacttat gtatacttct ctaaagattc ttagggcttg taagcaatga 300
ggtttaaggc natttttttag gatgttagca tcccggggct gacttngccg ggctgtggga 360
acccaggnc cgagtg 378

```

&lt;210&gt; 139

&lt;211&gt; 447

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(447)

<223> 5' terminal sequence. tek tyrosine kinase,  
endothelial (venous malformations, multiple  
cutaneous and mucosal) (TEK) gene.

&lt;400&gt; 139

```

gctttcactg gcatgggaga cccttgacac ctgctgagaa aacatgcctc tgccaaagga 60
tgtgatatat aagtgtacat atgtgctgta cacctgggac cttcaccact gtagatccca 120
tgcattgatac tatgtagtat gctctgactc taataggact gtatatactg ttttaagaat 180
gggctgaaat cagaatgcct gtttgtgggt tcatatgcaa taatatattt ttttaaaaat 240
gtggacttca taggaaggcg tgagtacaat tagtataatg cataactcat tgttgtccta 300
ggatattttg atatttacct ttatgttggg atgctattaa atgttttccn gtgtccaaag 360
taaaatattg ttttaaaaac ctaacaatgg accccgatag tacag ggtta agtgagggga 420
accttatgga ttctaacaag tcctagg 447

```

&lt;210&gt; 140

<211> 4138  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(4138)  
<223> tek tyrosine kinase, endothelial (venous  
malformations, multiple cutaneous and mucosal)  
(TEK) gene.

<400> 140  
cttctgtgct gttccttctt gcctctaact tgtaaacaag acgtactagg acgatgctaa 60  
tggaagtc acaaccgctg ggtttttgaa aggatccttg ggacctcatg cac atttgtg 120  
gaaactggat ggagagattt ggggaagcat ggactcttta gccagcttag ttctctgtgg 180  
agtcagcttg ctctttcttg gaactgtgga aggtgccatg gacttgatct tgatcaattc 240  
cctacctctt gtatctgatg ctgaaacatc tctcacctgc attgectctg ggtggcgccc 300  
ccatgagccc atcaccatag gaaggactt t gaagcctta atgaaccagc accaggatcc 360  
gctggaagt actcaagatg tgaccagaga atgggctaaa aaagtgtgtt ggaagagaga 420  
aaaggctagt aagatcaatg gtgcttattt ctgtgaagg cgagttcgag gagaggcaat 480  
caggatacga accatgaaga tgcgtcaaca agcttcttcc ctaccagcta ctttaactat 540  
gactgtggac aaggagagata acgtgaacat atctttcaaa aaggtattga ttaaagaaga 600  
agatgcagt atttacaaaa atggttctct catccattca gtgccccggc atgaagtacc 660  
tgatattcta gaagtacacc tgcctcatgc tcagcccag gatgctggag tgtactcggc 720  
caggtatata ggaggaaaacc tcttcacctc ggcttcacc aggctgatag t cgggagatg 780  
tgaagcccag aagtggggac ctgaatgcaa ccatctctgt actgcttgta tgaacaatgg 840  
tgtctgccat gaagatactg gagaatgcat ttgcctcct gggtttatgg gaaggacgtg 900  
tgagaaggct tgtgaactgc acacgtttgg cagaacttgt aaagaaagg gcagtgagaca 960  
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taagcttagg tgcagctgca acaatgggga gatgtgtgat cgcttccaag gatgtctctg 1140  
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gatagtggat ttgccagatc atatagaagt aaacagtggg aaatttaatc ccatttgcaa 1260  
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agatgacttt tatgttgaag tggagagaag gtctgtgcaa aaaagtgatc agcagaatat 1920  
taaagtcca ggcaacttga cttcgggtgct acttaacaac ttacatcca gggagcagta 1980  
cgtggtccga gctagagtca acaccaaggc ccagggggaa tggagtgaag atctcactgc 2040  
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accagctgtg cagtccaact cagggactct ggccctaaac aggaaggtca aaaacaacc 2580  
agatcctaca atttatccag tgcttgactg gaatgacatc aaatttcaag atgtgattgg 2640  
ggagggcaat ttggccaag ttcttaaggc gcgcatcaag aaggatgggt tacggatgga 2700  
tgctgccatc aaaaagaatga aagaatatgc ctccaaagat gatcacaggg actttgcagg 2760



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agaactggaa gttctttgta aacttgga ccatccaaac atcatcaatc tcttaggagc 2820
atgtgaacat cgaggctact tgtacctggc cattgagtag gcgccccatg gaaaccttct 2880
ggacttcctt cgcaagagcc gtgtgctgga gacggaccca gcatttgcca ttgccaata g 2940
caccgcgtcc aactgtcct cccagcagct ccttcacttc gctgccgacg tggcccgagg 3000
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gccccagggc tacagactgg agaagcccct gaactgtgat gatgaggtgt atgatctaata 3360
gagacaatgc tggcgggaga agccttatga gaggccatca ttgtcccaga tattggtgtc 3420
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gcacattgta aaaagtttta gttttgatga gttgtgagtt taccttgtat actgtaggca 4080
cactttgcac tgatatatca tgagtgaata aatgtcttgc ctactcaaaa aaaaaaaa 4138

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&lt;210&gt; 141

&lt;211&gt; 395

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(395)

<223> 3' terminal sequence. tumor necrosis factor  
receptor superfamily, member 6 (TNFRSF6) gene.

&lt;400&gt; 141

```

taattccaaa cacaaggggc aaaaaaatcc tccataaatg gaagttcttt aggtggttcc 60
aggnatctgc ttcagtttat aa ctatcttc acagtttaca ttacagaaa tataaatatt 120
atttcttaaa attcacattt aatacaaaact ttcaaagata tttaaacgta ggatagtagt 180
aaggagaatc ttaaacttta gaaacttggg ggtatgacaa gagcaattcc taaatccaga 240
tgatgatttt accattgcta tgtataagct gccatttgta ggcaggtttt acatggggac 300
attattgaac attttcgggg ggtgggggga aaaataaggn atctatttta tccatctttg 360
gattggcaaa cctgggggttc angacatgtt caca 395

```

&lt;210&gt; 142

&lt;211&gt; 461

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(461)

&lt;223&gt; 5' terminal sequence. tumor necrosis factor

receptor superfamily, member 6 (TNFRSF6) gene.

<400> 142

```
tcgtaattgg catcaacttc atggaaagaa agaagcgat gacacattga ttaaagatct 60
caaaaaagcc aatctttgta ctcttgag a gaaaattcag actatcatcc tcaaggacat 120
tactagtgc tcagaaaatt caaacttcag aaatgaaatc caaagcttg tctagagtga 180
aaaacaacaa attcagttct gagtatatgc aattagtgt tgaagagatt cttaatatgct 240
ggctgtaaat actgcttggt tttttactgg gtacatttta tcatttatta gcgctgaaga 300
gccacaatat ttgtagggtt ttaatatctc catggattct gcctccaagg gtgtttaaaa 360
tctagtgtgg ggaacaaac ttccttcaag ggttaaatgc ngtggcctgg ctaagtaccc 420
ccattaggga gtgtttgccg ggggttgnaa ggtttaggt t 461
```

<210> 143

<211> 2551

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(2551)

<223> tumor necrosis factor receptor superfamily,  
member 6 (TNFRSF6) gene.

<400> 143

```
gcaagagtga cacacaggtg ttcaaagacg cttctgggga gtgaggga g cggtttacga 60
gtgacttggc tggagcctca ggggcgggca ctggcacgga acacaccctg aggccagccc 120
tggctgcccc ggcgagctg cctcttctcc cgcgggttg tggaccgct cagtacggag 180
ttggggaagc tcttcaactt cggaggattg ctcaacaacc atgctgggca tctggaccct 240
cctacctctg gttcttacgt ctgttgct ag attatcgctc aaaagtgtta atgcccagt 300
gactgacatc aactccaagg gattggaatt gaggaagact gttactacag ttgagactca 360
gaacttgaa ggcctgcac atgatggcca attctgccat aagccctgtc ctccagggtga 420
aaggaaaagct agggactgca cagtcaatgg ggatgaacca gactgcgtgc cctgccaaga 480
aggggaaggag tacacagaca aagcccattt ttcttccaaa tgcagaagat gtagattgtg 540
tgatgaagga catggcttag aagtggaaat aaactgcacc cggaccaga ataccaagt 600
cagatgtaaa ccaactttt ttgttaactc tactgtatgt gaacactgtg accctgcac 660
caaatgtgaa catggaatca tcaaggaatg cacactcacc agcaacac ca agtgcagaaga 720
ggaaggatcc agatctaact tggggtggct ttgtcttctt cttttgccaa ttccactaat 780
tgtttgggtg aagagaaagg aagtacagaa aacatgcaga aagcacagaa aggaaaacca 840
aggttctcat gaatctccaa ccttaaatcc tgaacacagt gcaataaatt tatctgatgt 900
tgacttgagt aaatatatca ccaacta ttgc tggagtcagt aactaagtc aagttaaagg 960
ctttgttoga aagaatggtg tcaatgaagc caaaatagat gagatcaaga atgacaatgt 1020
ccaagacaca gcagaacaga aagttcaact gcttcgtaat tggcatcaac ttcatggaaa 1080
gaaagaagcg tatgacacat tgattaaaga tctcaaaaaa gccaatctt gtactcttgc 1140
agagaaaatt cagactatca tcctcaagga cttactagt gactcagaaa attcaaaact 1200
cagaaatgaa atccaaagct tggctagag tgaaaaaaca caaattcagt tctgagtata 1260
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gattatgctc tggcatctaa catatgattc tgtagtatga atgtaatcag tgtatgttag 1560
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acagtttatt ggtgtcatat tatacaatat ttcaatttg aattcacata gaaaacatta 1860
aattataatg ttgactatt atatatgtgt atgcatttta ctggctcaa actacctact 1920
tctttctcag gcatcaaaag ctttttgagc aggagagtat tactagagct ttgccacctc 1980
```

```

tccatttttg ccttggtgct catottaat g gcctaata gca cccccaaaca tggaaatata 2040
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tttgagagata ctaactgctc tcagagaaag tagctttgtg acatgtcatg aacccatgtt 2160
tgcaatcaaa gatgataaaa tagattctta tttttccccc acccccgaag atgttcaata 2220
atgtcccatg taaaacctgc tacaaatggc agcttataca tagcaatggg aaaatcatca 2280
tctggattta ggaattgctc ttgtcatacc cccaagtctc taagatttaa gattctcctt 2340
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aatatttata tttctgtaaa tgtaactgt gaagatagtt at aaactgaa gcagatacct 2460
ggaaccacct aaagaacttc catttatgga ggattttttt gccccttggtg tttggaatta 2520
taaaatatag gtaaaagtac gtaattaaat a 2551

```

&lt;210&gt; 144

&lt;211&gt; 434

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(434)

<223> 3' terminal sequence. cyclin -dependent  
kinase inhibitor 1a (p21, cip1) (CDKN1A) gene.

&lt;400&gt; 144

```

aaagtcacta agaatacttt atnagcacc tgctgtatat tcagcattgt gggaggagct 60
gtgaaagaca cagaacagta cagggtgtgg tccctgccct cgagagggtt acagtctagg 120
tgagagaaac ggaaccagga cacatgggga gccgagagaa aacagtccag gccagtatgt 180
tacaggagct ggaaggtnnt tggggtcaga cccaataact ccaagtacac taagcacttc 240
agtccttcca ggggtcaaac gttagtgccg gaaagacaa ctactcccag ccccatatga 300
gcccacgtgg catgccctgt ccatagcctc tactgccacc atcttaaaat gtctgactcc 360
ttgttcgct ggctaattca aagtgaatg aactggggag ggatgggggt gatgaggaag 420
gttcgntgga cggt 434

```

&lt;210&gt; 145

&lt;211&gt; 257

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(257)

<223> 5' terminal sequence. cyclin -dependent  
kinase inhibitor 1a (p21, cip1) (CDKN1A) gene.

&lt;400&gt; 145

```

cttgtgtgc ntncagggg a gcaggctgaa ggggtccccag gtggacctgg agactctcag 60
ggtcgaaaac ggcggcagac cagcatgaca gatttctacc actccaaacg ccggctgac 120
ttctccaaga ggaagcccta atccgccac aggaagcctg cagtccctga agcgcgagg 180
cctcaaaggc cntnctnaca tcttctgcct tagtctcagt ttgtgtgtct taattattat 2 40
ttgtgtttta aattttt 257

```

&lt;210&gt; 146

&lt;211&gt; 2121

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2121)

<223> cyclin-dependent kinase inhibitor 1a (p21,  
cip1) (CDKN1A) gene.

&lt;400&gt; 146

```
gccgaagtca gttccttgtg gagccggagc tgggcgcgga ttgcgccagg caccgaggca 60
ctcagaggag gcgcatgtc agaaccggct ggggatgtcc gtcagaacct atgcgcgagc 120
aaggcctgcc gcgcctctt cggcccagtg gacagcgagc agctg agccg cgactgtgat 180
gcgctaattg cgggctgcat ccaggaggcc cgtgagcgat ggaacttcga ctttgtcacc 240
gagacaccac tggagggtga cttgccttg gagcgtgtgc ggggccttgg cctgcccagg 300
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gtatatgatg gggagtaga tctttctagg agggagacac tggccctca aatcgtccag 1680
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cacctagact gtaaacctct cgagggcgag gaccacaccc tgtactgttc tgtgtctttc 2040
acagctcttc ccacaatgct gaataacag caggtgtctc ataatgatt cttagtgtgact 2100
ttaaaaaaaa aaaaaaaaaa a                                     2121
```

&lt;210&gt; 147

&lt;211&gt; 452

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

<222> (1)..(452)

<223> 3' terminal sequence. phospholipase a2,  
group iia (platelets, synovial fluid) (PLA2G2A)  
gene.

<400> 147

```
gatttgctaa ttgctttatt cagaagagac cccccggagt acagcttctt tggtaagca 60
cggagttgag gtggaggaga gcagtagaag gctggaaatc tgctggatgt ctcatcttg 120
gtgggtatag aagggtcctt gcctggcctc taggatgggt gagggatgct ttctgcatgg 180
ccaaggaaact tggtagggt agggaggag ggtatgagag agggaaattc agcactgggt 240
ggaaggtttc cagggaagag gggactcagc aacgaggggt gtcacctctg cagtntttat 300
tggaatagta ctggtacttt ttattgtagg tctcttntt tctagcaaaa cagggtngca 360
gcagccttat cacacttcac acagttgact tctgcaggag tcccntttt gcacaggttg 420
attctgctcc ccgaagttac taaacttttt tt 452
```

<210> 148

<211> 379

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(379)

<223> 5' terminal sequence. phospholipase a2,  
group iia (platelets, synovial fluid) (PLA2G2A)  
gene.

<400> 148

```
tggagtcttc tgagagagcc accaaggagg agcaggggag cgacggccgg ggcagaagtt 60
gagaccaccc agcagaggag ctaggccagt ccatctgc at ttgtcaccca agaactctta 120
ccatgaagac cctctactg ttggcagtga tcatgatctt tggcctactg caggcccatg 180
ggaatttggt gaatttcac agaatgatca agttgacgac aggaaggaa gccgcactca 240
gttatggctt ctacggctgc cactgtggcg tgggttgagc aggatcccc aaggatgcaa 300
cggattcgct gctgtg tcatgactgt ttgctacaaa cgtctgggag aaacgtgggt 360
tnttggcacc aaatttttt 379
```

<210> 149

<211> 854

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(854)

<223> phospholipase a2, group iia (platelets,  
synovial fluid) (PLA2G2A) gene.

<400> 149

```
gaattcccaa ctctggagtc ctctgagaga gccaccaagg aggagcaggg gagcgacggc 60
cggggcagaa gttgagacca ccagcagag gagctaggcc agtccatctg catttgtc ac 120
ccaagaactc ttacatgaa gaccctccta ctgttggcag tgatcatgat ctttggccta 180
ctgcaggccc atgggaattt ggtgaatttc cacagaatga tcaagttgac gacaggaaag 240
gaagccgcac tcagttatgg cttctacggc tgccactgtg gcgtgggtgg cagaggatcc 300
```

```
cccaaggatg caacggatcg ctgctgtgtc actcat gact gttgctacaa acgtctggag 360
aaacgtggat gtggcaccaa atttctgagc tacaagttta gcaactcggg gacgagaatc 420
acctgtgcaa aacaggactc ctgcagaagt caactgtgtg agtgtgataa ggctgtgcc 480
acctgttttg ctagaacaa gacgacctac aataaaaagt accagtacta ttccaataaa 540
cactgcagag ggag cacccc tcgttgctga gtccctctt ccctggaaac ctccacca 600
gtgctgaatt tccctctctc ataccctccc tccctaccct aaccaagttc cttggccatg 660
cagaaagcat ccctcaccca tcctagaggc caggcaggag cccttctata cccaccaga 720
atgagacatc cagcagattt ccagccttct actgctctcc tccacctcaa ctccgt gctt 780
aaccaaagaa gctgtactcc ggggggtctc ttctgaataa agcaattagc aaatcaaaaa 840
aaaaaaagga attc 854
```

<210> 150

<211> 224

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:p rimer

<220>

<221> misc\_feature

<222> (1)..(224)

<223> 3' terminal sequence.

glyceraldehyde-3-phosphate dehydrogenase (GAPD)  
gene.

<400> 150

```
ggttgagcac aggnacttt attgatgna catgacaagg tgcggctccc taggcccctc 60
ccctnttcaa ggggtctaca tggcaact nt gaggagggga gattcagtgt ggtgggggac 120
tgagtntggc agggactccc cagcagttag ggtctctctc ttctcttnt gctcttntg 180
gggntggtgg nccagggn tn ttactccttg gaggccatnt gggc 224
```

<210> 151

<211> 359

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(359)

<223> 5' terminal sequence.

glyceraldehyde-3-phosphate dehydrogenase (GAPD)  
gene.

<400> 151

```
gcgctgagta cgtcgtggag tcactggcg tcttcaccac catggagaag gctggggctc 60
atttgcaggg gggagccaaa agggatcatc tcttgcccc ctctgctgat gccccatgt 120
tcgtcatggg tgtgaaccat gagaagtatg acaacagcct caagatcatc agcaatgcct 180
cctgcaccac caactgctta gacccctgg gccaaagtca tccatgacaa ctttggatc 240
gtggaaggac tcatgaccac agtccatgcc atcactgcca c ccagaagac tgtggatggc 300
ccctncggga aactgtgggc gtgatggccg cggggttctt tcagaacatc atccctgcc 359
```

<210> 152

<211> 1283

<212> DNA/RNA

102/292

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1283)

<223> glyceraldehyde -3-phosphate dehydrogenase  
(GAPD) gene.

&lt;400&gt; 152

```
ctctctgctc ctctgttcg acagtcagcc gcatcttctt ttgcgtcgcc agccgagcca 60
catcgctcag acaccatggg gaaggtgaag gtccgagtcac acggatttgg tcgtattggg 120
cgccctgtgc ccagggtctg ttttaactct ggta aagtgg atattgttgc catcaatgac 180
cccttcattg acctcaacta catggtttac atgttccaat atgattccac ccatggcaaa 240
ttccatggca ccgtcaaggc tgagaacggg aagcttgtca tcaatggaaa tcccatcacc 300
atcttccagg agcgagatcc ctccaaaatc aagtggggcg atgctggcgc tgagtaogtc 360
gtggagtcca ctggcgtctt caccaccatg gagaaggctg gggctcattt gcagggggga 420
gccaaaaggg tcatcatctc tgccccctct gctgatgccc ccatgttctg catgggtgtg 480
aaccatgaga agtatgacaa cagcctcaag atcatcagca atgcctcctg caccaccaac 540
tgcttagcac ccctggccaa ggtcatccat gacaactttg gtatcgtgga agga ctcatg 600
accacagtcc atgccatcac tgccacccag aagactgtgg atggccctc cgggaaactg 660
tggcgtgatg gccgcggggc tctccagaac atcatccctg cctctactgg cgctgccaag 720
gctgtgggca aggtcatccc tgagctgaac ggggaagtca ctggcatggc cttccgtgtc 780
cccactgcca acgtgtcagt ggtggacctg ac ctgccgtc tagaaaaacc tgccaaatat 840
gatgacatca agaaggtggt gaagcaggcg tcggaggggc ccctcaaggg catcctgggc 900
tacactgagc accaggtggt ctctctgac ttcaacagcg acaccactc ctccacctt 960
gacgctgggg ctggcattgc cctcaacgac cactttgtca agctcattc ctggtatgac 1020
aacgaatttg gctacagcaa cagggtggtg gacctcatg gccacatggc ctccaaggag 1080
taagaccctt ggaccaccag cccagcaag agcacaagag gaagagagag accctcactg 1140
ctggggagtc cctgccacac tcagtcccc accacactga atctccctc ctacagtgtg 1200
ccatgtagac ccctgaaga ggggaggggc ctaggagacc gcacctgt c atgtaccatc 1260
aataaagtac cctgtgctca acc                                     1283
```

&lt;210&gt; 153

&lt;211&gt; 361

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(361)

<223> 3' terminal sequence. jun b proto -oncogene  
(JUNB) gene.

&lt;400&gt; 153

```
tacttaata gattcaatan aaagaacaaa cacacacaaa cacaacacg tcttaaaata 60
aactctttag agactaagtg cgtgtttctt ttccacagta cgggtgcagag aggggagggc 120
agggggcggg ggtcccttcc caatgtcccc gcggtcttga gta ccaggcg gcggggccag 180
ctccnant ncgccccctc ttccccctcc tgttaaatac acaaataat tatattcaat 240
ntgaatcgng tctntttcca gcagaaaaaa aacatacaaa aaaaagtggg aagggggggg 300
cttntttaa cgttcggang ttggaaggnc tttggggcnc aggggtaggg angggccgag 360
t                                     361
```

&lt;210&gt; 154

<211> 401  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(401)  
<223> 5' terminal sequence. jun b proto-oncogene  
(JUNB) gene.

<400> 154  
agcgcatcaa agtngagcgc angccttgcg gaaccggctn gcggccacca agtgccggaa 60  
gcggaantgg gagcgcatcg ggcttgggag gacaagggtga agacgctcaa ggccgagaac 120  
gcgggngtgt cgagtaccgc cggttctctc cgggagcagg tggcccagct caaacagaag 180  
gtcatgacct acgtnagc aa cggctntnag ctgctgcttn gggtaaggga acacgccttc 240  
tggaacgttc cctgccccctt tacgggacac ccccttcgtt tnggacggtt nggcacacgg 300  
tttcccactn ggggtccagg gtagcaggcg gtggggnacc cacctggggg acntaggggg 360  
cgnccgcaaa ccacattngg atttccggcc ttcttaacct t 401

<210> 155  
<211> 1797  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(1797)  
<223> jun b proto-oncogene (JUNB) gene.

<400> 155  
ccagcaggga gctgggagct gggggaaacg acgc caggaa agctatcgcg ccagagaggg 60  
cgacgggggc tcgggaagcc tgacagggtt ttgcgacaca gctgccggtt ggctgctacc 120  
cgcccgcgcc agcccccgag aacgcgcgac caggcaccca gtccgggtcac cgcagcggag 180  
agctcgcgcg tcgctgcagc gagggccgga gcggcccgcc agggaccctc cccagaccgc 240  
ctggggccgcc cggatgtgca ctaaaatgga acagcccttc taccacgacg actcatacac 300  
agctacggga tacggccggg cccctggtgg cctctctcta cagactaca aactcctgaa 360  
accgagcctg gcggtcaacc tggccgaccc ctaccggagt ctcaaagcgc ctggggctcg 420  
cggaccgggc ccagagggcg gcggtggcgg cagctacttt tctggtcagg gctcg gacac 480  
cggcgcgtct ctcaagctcg cctcttcgga gctggaacgc ctgattgtcc ccaacagcaa 540  
cggcgtgata acgacgacgc ctacaccccc gggacagtac ttttaccccc gcgggggtgg 600  
cagcgttgga ggtgcagggg gcgcaggggg cggcgtcacc gaggagcagg agggcttcgc 660  
cgacggcttt gtcaaagccc tggacgatct gca caagatg aaccacgtga cccccccaa 720  
cgtgtccctg ggcgctaccg gggggccccc ggtggggccc gggggcgtct acgccggccc 780  
ggagccacct cccgtttaca ccaacctcag cagctactcc ccagcctctg cgtcctcggg 840  
aggcgcgggg gctgcgctcg ggaccgggag ctggtaccgc acgaccacca tcagctacct 900  
cccacacgcg ccgcctctcg ccggtggcca cccggcgag ctgggcttgg gccgcggcgc 960  
ctccaccttc aaggaggaac cgcagaccgt gccggaggcg cgcagccggg accccacgcc 1020  
gccggtgttc cccatcaaca tgaagacca agagcgcata aaagtggagc gcaagcggct 1080  
gcgggaaccg ctggcgccca ccaagtgcgg gaagcggaag ctggagcgca t cgcgcgcct 1140  
ggaggacaag gtgaagacgc tcaaggccga gaacgcgggg ctgtcgagta ccgcggcct 1200  
cctccgggag caggtggccc agctcaaaca gaaggtcatg acccacgtca gcaacggctg 1260  
tcagctgctg cttgggggtca agggacacgc cttctgaacg tcccctgcc ctttacggac 1320  
acccctcgcg ttggacggct ggacac acgc ctcccactgg ggtccaggga gcaggcgggtg 1380  
ggcaccacac ctgggacctt ggggcgcgcg aaaccacact ggactccggc cccctaccc 1440



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tgcgcccagt ccttccacct cgacgtttac aagccccccc ttccactttt ttttgtatgt 1500  
tttttttctg ctggaacacag actcgattca tattgaatat aatataattg tgtatttaac 1560  
agggagggga agagggggcg atcgggcg agctggcccc gccgcctggt actcaagccc 1620  
gcggggacat tgggaagggg acccccgcct cctgccctcc cctctctgca ccgtactgtg 1680  
gaaaagaaac acgcacttag tctctaaaga gtttatttta agacgtgttt gtgtttgtgt 1740  
gtgtttgttc tttttattga atctatttaa gtaaaaaaaaa aattggttct ttattaa 1797

&lt;210&gt; 156

&lt;211&gt; 335

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(335)

<223> 3' terminal sequence. cellular retinoic  
acid-binding protein 2 (CRABP2) gene.

&lt;400&gt; 156

aagcatttta ataaaattaa caaataaata ttctaaactg tataggctac agggacaaaag 60  
ggtagaagct agagggccag tctttctgctc tcaggccctc aagtcctctt tagagagacc 120  
ctgctctggg ctggtttggg gctaggactg ctgacttggg gaggcgggga gtgaaccggg 180  
aatgggtgat ctgggctctt gcagccattc ctctttgttg gtgtagggga ggagagaaga 240  
ggtcaaagaa agcaagaccc tgcaagaggc atcccagtga cccccagaag tgactggggg 300  
aaggggagcg ctatcctagg anggtggggg tgggt 335

&lt;210&gt; 157

&lt;211&gt; 481

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(481)

<223> 5' terminal sequence. cellular retinoic  
acid-binding protein 2 (CRABP2) gene.

&lt;400&gt; 157

gcctggactt gtcttggggt ccagaacctg acgaccgggc gacgcgacgt ctct ttgac 60  
taaaagacag tgtccagtgc tccagcctag gagtctacgg ggaccgcctc ccgcgccgcc 120  
accatgccca acttctcttg caactggaaa atcatccgat cggaaaactt cgaggaattg 180  
ctcaaagtgc tnggggtgaa tgtgatgctg aggaagattg ctgtggctnc agcgtccaag 240  
ccagcagtng agatcaaaca ggaggagac act ttctaca tcaaaacctc caccaccgtg 300  
cggcaccaca gagattaact tcaagggtng ggaggagttt gagggagcag antgtgggtg 360  
gggaggccct gttaaggagc ngggtgaaat ggggagagtg aggattaaat ggtcttttga 420  
gcagaagttc ctgaaggng aggggccccca agacntcttg gacngagaa tttccccacg 480  
t 481

&lt;210&gt; 158

&lt;211&gt; 969

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(969)

<223> cellular retinoic acid-binding protein 2  
(CRABP2) gene.

&lt;400&gt; 158

```
agctttgagg ttgtccctgg acttgtcttg gttccagaac ctgacgaccc ggcgacggcg 60
acgtctcttt tgactaaaag acagtgtcca gtgctccagc ctaggagtct acgggggaccg 120
cctcccgcg cgcaccatg cccaacttct ctggcaactg gaaaatcatc cgatcggaaa 180
acttcgagga attgctcaaa gtgctggggg tgaatgtgat gctgaggaag attgctgtgg 240
ctgcagcgta caagccagca gtggagatca aacaggaggg agacactttc tacatcaaaa 300
cctccaccac cgtgcgcacc acagagatta acttcaagggt tggggaggag tttgaggagc 360
agactgtgga tgggaggccc tgtaagagcc tggtgaaatg ggagag tgag aataaaatgg 420
tctgtgagca gaagctcctg aaggagagg gccccaagac ctcgtaggac agagaactga 480
ccaacgatgg ggaactgatc ctgaccatga cggcggatga cgttgtgtgc accaggggtct 540
acgtccgaga gtgagtggcc acaggtagaa ccgcggccga agcccaccac tggccatgct 600
caccgcctg cttcactgcc ccct ccgtcc caccctctcc ttctaggata gcgctcccct 660
taccacagtc acttctgggg gtcactggga tgcctcttgc agggctctgc tttctttgac 720
ctcttctctc ctcccctaca ccaacaaaga ggaatggctg caagagccca gatcacccat 780
tccgggttca ctcccgcct cccaagtca gcagtcctag ccccaaacca gccagagca 840
gggtctctct aaaggggact tgagggcctg agcaggaaa actggccctc tagcttctac 900
cctttgtccc tgtagcctat acagtttaga atatttattt gttaatttta ttaaaatgct 960
ttaaaaaaa
```

&lt;210&gt; 159

&lt;211&gt; 344

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(344)

<223> 3' terminal sequence. activin a receptor  
type ii-like 1 (ACVRL1) gene.

&lt;400&gt; 159

```
cgcggnrtga ggggaggtgg ccccgntcc gccgangaan tcgccccg cc acccgagag 60
cncncagagg gaccattgac cttgggtcc ccaggaaaag gccttctgat gctgctgatg 120
gccttggtga ccagggaga ccctgtgaag ccgtctcggg gcccgctggt gacctgcacg 180
tgtgagagcc cacattgcaa ggggcctacc tgccgggggg cctgggtgca cagtagtgct 240
tgggtgcggg aggaggggag gcacccc cag ggaacattcg gggntgcggg aantttgcac 300
agggagntct tgcagggggg gcgccccacc gatttcgttc aacc 344
```

&lt;210&gt; 160

&lt;211&gt; 416

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(416)  
<223> 5' terminal sequence. activin a receptor  
type ii-like 1 (ACVRL1) gene.

<400> 160  
gtcagtctcc cggaaccagg actgttcac cctcgaggag aagatcttga cggccacact 60  
ctcaccgtgc cacaagcccc gccacacttc gccatagcgc cttttccac acactccacc 120  
aaggcaacct gccgtngcca ctgtcctctg caccaggga ggggagccct gagccactcc 180  
ctgtgggtgg cagtcaactgt ccaggagggt cccccaacat gctgttcgcc ctgcttcaga 240  
tgcttttcag ggatgaggat gggattttcc cagcttcgct gttgcagggc caggttgctt 300  
tttccttgcc tncgttcggg acatggccac agggcccagg ggacaaccag g gggccacca 360  
gggggnccag gcaanggcca agncacgggg ggcccagggt ttnaaggggc cagttt 416

<210> 161  
<211> 1970  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(1970)  
<223> activin a receptor type ii-like 1 (ACVRL1)  
gene.

<400> 161  
aggaacacgggt ttattaggag ggagtgggtg agctgggcca ggcaggaaga cgctggaata 60  
agaaacattt ttgtccagc ccccatccca gtcccgggag gctgccgcgc cagctgcgcc 120  
gagcgagccc ctcccgggt ccagcccgggt ccggggccgc gccggacc c agcccgggt 180  
ccagcgctgg cggtgcaact cggcccgccg ggtggagggg aggtggcccc ggtccgccga 240  
aggctagcgc cccgccacce gcagagcggg cccagaggga ccatgacctt gggctcccc 300  
aggaagggcc ttctgatgct gctgatggcc ttggtgacct agggagacct tgtgaagccg 360  
tctcggggcc cgtcgttgac ctgcacg tgt gagagcccac attgcaagg gcctacctgc 420  
cggggggcct ggtgcacagt agtctggtg cgggaggagg ggaggcacc ccaggaacat 480  
cggggctgcg ggaacttgca cagggagctc tgcagggggc gccccaccga gttcgtcaac 540  
cactactgct gcgacagcca cctctgcaac cacaacgtgt cctggtgct ggaggccacc 600  
caacctcctt cggagcagcc gggaacagat ggccagctgg ccctgatcct gggccccgtg 660  
ctggccttgc tggccctgggt ggccctgggt gtccctgggc tgtggcatgt ccgacggagg 720  
caggagaagc agcgtggcct gcacagcgag ctgggagagt ccagtctcat cctgaaagca 780  
tctgagcagg gcgacacgat gttgggggac ctccctggaca gtgactg cac cacagggagt 840  
ggctcagggc tccccttctt ggtgcagagg acagtggcac ggcaggttgc cttggtggag 900  
tgtgtgggaa aaggccgcta tggcgaagtg tggcggggct tgtggcacgg tgagagtgtg 960  
gccgtcaaga tcttctctc gagggatgaa cagtccctgg tccgggagac tgagatctat 1020  
aacacagtat tgctcagaca cgac aacatc ctaggcttca tgcctcaga catgacctcc 1080  
cgcaactcga gcacgcagct gtggctcatc acgcactacc acgagcacgg ctccctctac 1140  
gactttctgc agagacagac gctggagccc catctggctc tgaggctagc tgtgtccgcg 1200  
gcatgcggcc tggcgacact gcacgtggag atcttcggta cacagggcaa accagccatt 126 0  
gccaccgcg acttcaagag ccgcaatgtg ctggtcaaga gcaacctgca gtgttgcac 1320  
gccgacctgg gcctggctgt gatgcactca cagggcagcg attacctgga catcggaac 1380  
aaccgagag tgggcaccaa gcggtacatg gcaccgagg tgctggacga gcagatccgc 1440  
acggactgct ttgagtcta caagtggact gacatctg gg cctttggcct ggtgctgtg 1500  
gagattgccc gccggaccat cgtgaatggc atcgtggagg actatagacc acccttctat 1560  
gatgtggtgc ccaatgacct cagctttgag gacatgaaga aggtggtgtg tgtggatcag 1620  
cagaccccca ccatccctaa ccggttggt gcagaccgg tccctcagc cctagctcag 1680  
atgatcggg agtgctggt cccaaacccc tctgcccagc tcaccgcgct gcggatcaag 1740  
aagacactac aaaaaattag caacagtcca gagaagccta aagtgattca atagcccagg 1800

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agcacctgat tcctttctgc ctgcaggggg ctgggggggt ggggggcagt ggatgggtgcc 1860  
ctatctgggt agaggtagtg tgagtgtggt gtgtgctggg gatgggcagc t gcgcctgcc 1920  
tgctcggccc ccagcccacc cagccaaaaa tacagctggg ctgaaacctg 1970

&lt;210&gt; 162

&lt;211&gt; 407

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(407)

<223> 5' terminal sequence. lim domain protein  
(RIL) gene.

&lt;400&gt; 162

gtgacctgc gcgggccttc gccctggggc ttccgcctgg tngggccgng gacttcagcg 60  
cgcccctcac catctcacgg gtccatgctg gcagcaaggc tcatntggct gccctgtgcc 120  
caggagacct gatccaggcc atcaatggtg agagcacaga gctcatgac a cacctggang 180  
cacagaaccg catcaagggc tgccacgac acctcacact gtctgtgagc aggcctgagg 240  
gcaggagctg gccagtgcc cctgatgaca gcaagggtca ggcacacagg atccacatcg 300  
ntcctgagat ccaggacggc agcccaacaa ccagcaggcg gccctcaggc accgggactt 360  
gggccagaag atnnggcagan caagnct ggg gtttttncat atggaca 407

&lt;210&gt; 163

&lt;211&gt; 1130

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1130)

&lt;223&gt; lim domain protein (RIL) gene.

&lt;400&gt; 163

tgagagtccg gctcaggctc cggctgcggc tccagcccgc gatgcccacat tccgtgaccc 60  
tgcgcgggcc ttccgcctgg ggcctccgcc tgggtgggccc ggacttcagc gcgcccctca 120  
ccatctcacg ggtccatgct ggcagcaagg cctcattggc tgccctgtgc ccaggagacc 180  
tgatccaggc catcaatggt gagagcacag agctcatgac acacctg gag gcacagaacc 240  
gcatcaaggc ctgccacgat cacctcacac tgtctgtgag caggcctgag ggcaggagct 300  
ggcccagtg cctgatgac agcaaggctc aggcacacag gatccacatc gatcctgaga 360  
tccaggacgg cagcccaaca accagcaggc ggccctcagg caccgggact gggccagaag 420  
atggcagacc aagcctggga tctcc atatg gaaaaccccc ttgctttcca gtccctcaca 480  
atggcagcag cgaggccacc ctgccagccc agatgagcac cctgcatgtg tctccacccc 540  
ccagcgctga ccagcagag gcctcccgcg gagccgggag cagagtcgac ctgggctccg 600  
agggtgtacag gatgtgcgg gagccggccg agcccggtggc cgcggagccc aagcagtcag 660  
gctccttcgc ctacttgtag ggcattgtag aggcggcgca gggcggggat tggcccgggc 720  
ctggcgggcc ccggaacctc aagccacagg ccagcaagct gggcgctccg ctgagcggcc 780  
tgcaggggct gcccgagtgc acgcgtgct gccacggaat cgtgggcacc atcgtcaagg 840  
aacgggacaa gctctaccat cccgagtgtc tcatgtgcag tgact gcggc ctgaacctca 900  
agcagcgtgg ttacttcttt ctggacgagc ggctctactg tgagagccac gccaaaggcg 960  
gcgtgaagcc gcccgagggc tacgacgtgg tggcggtgta ccccaatgcc aaggtggaac 1020  
tcgtctgagc tgggacctg ctcccacccc tgcttcttaa ggtccctgct cggccgggtg 1080

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aaatatgttt caccctgtcc c tctaataaa gtcctctgtc tcaaaaaaaaa

1130

&lt;210&gt; 164

&lt;211&gt; 310

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(310)

&lt;223&gt; 5' terminal sequence. shc (src homology 2 domain-containing) transforming protein 1 (SHC1) gene.

&lt;400&gt; 164

anattcgga cgagggatcc ctctatgtc aacgtccaga acctagacaa ggcccggcaa 60  
gcagtgggtg gtgctgggcc cccaatcct gctatcaatg gcagtgcacc ccgggacctg 120  
tttgacatga agccttcga agatgctctt cgctgc ctc cacctcccca gtcggtgtcc 180  
atgntcagc agctccgagg ggagccctgg gttccatggg aagctgagcc ggcgggaggc 240  
tgaggcactg ctggcagctt caatgggat ttcnggtac gggagagcac gaccacacng 300  
gggcaatatg 310

&lt;210&gt; 165

&lt;211&gt; 3664

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(3664)

&lt;223&gt; shc (src homology 2 domain -containing) transforming protein 1 (SHC1) gene.

&lt;400&gt; 165

atggggcctg aaactgtctg ggtctgagct ggggagcgga agccacttgt ccctctccct 60  
ccccaggact tctgtgactc ctgggccaca gaggtccaac cagggttaagg gcctggggat 120  
accctctgcc tggccccctt gcccaaactg gcaggggggc caggctgggc agcagccct 180  
ctttcacctc aactatggat ctctgcccc ccaagcccaa gtacaatcca ct ccggaatg 240  
agtctctgtc atcgctggag gaaggggctt ctgggtccac cccccggag gagctgcctt 300  
ccccatcagc ttcattccctg ggccccatcc tgctcctct gctggggac gatagtcca 360  
ctaccctgtg ctctctcttc ccccgatga gcaacctgag gctggccaac ccgctgggg 420  
ggcgccagg gtctaagggg gagccaggaa gggcagctga tgatggggag gggatcgatg 480  
gggcagccat gccagagtca ggccccctac cctcctcca ggacatgaac aagctgagtg 540  
gaggcgggcg gcgcaggact cgggtggaag ggggccagct tggggcgag gagtggaccc 600  
gccacgggag ctttgtcaat aagcccacgc ggggctggct gcatcccaac gacaaagtca 660  
tgggaccggg ggttctctac ttggttcggt acatgggttg tgtggaggtc ctccagtcaa 720  
tgctgtccct ggacttcaac acccgactc aggtcaccag ggaggccatc agtctggtgt 780  
gtgaggctgt gccgggtgct aagggggcga caaggaggag aaagccctgt agccgcccgc 840  
tcagctctat cctggggagg agtaacctga aatttctggt aatgccaatc actctcaccg 900  
tctccaccag cagcctcaac ctcatggccg cagactgcaa acagatcatc gccaacacc 960  
acatgcaatc tatctcattt gcatccggcg gggatccgga cacagccgag tatgtcgct 1020  
atgttgccaa agaccctgtg aatcagagag cctgccacat tctggagtgt ccgaagggc 1080  
ttgccaggga tgcatcagc accattg gcc aggccttcga gttgcgcttc aaacaatacc 1140

109/292

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tcaggaaccc acccaactg gtcacccctc atgacaggat ggctggcttt gatggctcag 1200
catgggatga ggaggaggaa gagccacctg accatcagta ctataatgac ttcccgggga 1260
aggaaccccc cttggggggg gtggtagaca tgaggcttcg ggaaggagcc gctccagggg 1320
ctgctcgacc cactgcaccc aatgccaga cccccagcca cttgggagct acattgcctg 1380
taggacagcc tgttggggga gatccagaag tccgcaaaca gatgccacct ccaccacct 1440
gtccaggcag agagcttttt gatgatccct cctatgtcaa cgtccagaac ctagacaagg 1500
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tggacctga ggggtgtggt cggactaagg atcaccgctt tgaaagtgtc agtcacctta 1860
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caatcctttc caccctattc cctaactctc gggacctcgt ttgggagtgt tctgtgggct 2040
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cctctcaaca ccgccccccc ccatgtttaa actttgtgcc tttagaccatc tcttaggtct 2400
aatgatattt tatgcaaaca gttcttgga cctgaattc ttcaatgaca gggatgccaa 2460
caccttcttg gcttctggga cctgtgttct tgctgagcac cctctccggt ttgggttggg 2520
ataacagagg caggagtggc agctgtcccc tctccctggg gatatgcaac ccttagagat 2580
tgccccagag ccccaactccc ggccaggcgg gagatggacc cc tcccttgc tcagtgcctc 2640
ctggccgggg ccctcacccc caaggggtct gtatatacat ttcataaggc ctgccctccc 2700
atgttgcatg cctatgtact ctgcgcaaaa gtgcagccct tccctctgaa gcctctgcc 2760
tgctccctt tctgggaggg cggggtgggg gtgactgaat ttgggcctct tgtacagtta 2820
actctccag gtgatt ttgagggtgag aaaaggggca ttgagactat aaagcagtag 2880
acaatcccc cataccatct gttaggttgg aactgcattc ttttaaagtt ttatatgcat 2940
atatttttag gctgctagac ttactttcct attttctttt ccattgctta ttcttgagca 3000
caaaatgata atcaattatt acattttata atcacctttt tgacttttcc aagccc tttt 3060
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ccagagacct gaggcagatg aaattttatt ccatctagga ctagaaaaac ttgggtctct 3180
taccgcgaga ctgagaggca gaagtcagcc cgaatgcctg tcagtttcat ggaggggaaa 3240
cgcaaaacct gcagttcctg agtaccttct acaggcccg cccagcctag gccgggggtg 3300
gccacaccac agcaagccgg cccccctct tttggccttg tggataagg agagttagcc 3360
gttttcatcc tggcctcctt ttgctgtttg gatgtttcca cgggtctcac ttataccaaa 3420
gggaaaactc ttcattaaag tccgtatttc ttctaaaaaa aaaaaaaaaa aaatacat 3480
atacatcacc tttttgactt ttccaagccc ttttacagct cttggcattt tctcgccta 3540
ggcctgtgag gtaactggga tcgcaccttt tataccagag acctgaggca gatgaaattt 3600
atttccatct aggactagaa aaacttgggt ctcttaccgc gagactgaga ggcagaagtc 3660
agcc 3664

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&lt;210&gt; 166

&lt;211&gt; 449

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(449)

&lt;223&gt; 3' terminal sequence.

glyceraldehyde-3-phosphate dehydrogenase ( GAPD)  
gene.

&lt;400&gt; 166

110/292

gagcacaggg tnttttattg atggtacatg acaagggtgcg gctccctagg cccctcccct 60  
cttcaagggg tctacatgga aactgtgagg aggggagatt cagtgtggtg ggggactgag 120  
tntggcaggg actccccagc agtgagggtc tctctcttcc tcttgtgctc ttgctggggc 180  
tggtggtcca ggggtcttac tcttggagg ccatgtgggc atgagggtcca ccacctgtt 240  
gctgtagcca aattcgttgt cataccaggg aaatgagctt gacaaagtgg tcgttgaggg 300  
caatgccagc cccagccttc gaaggtggag gantgggtt cgctnttgaa gtcagaggag 360  
accacctggg tgctcagttt agcccagga tgcccttgag ggggccctcc gacgttt ttt 420  
tcaccacctt tttgatntca tcatnttt 449

&lt;210&gt; 167

&lt;211&gt; 467

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(467)

&lt;223&gt; 5' terminal sequence.

glyceraldehyde -3-phosphate dehydrogenase (GAPD)  
gene.

&lt;400&gt; 167

tggtcgacag tcagccgcat cttcttttgc gtcgccagcc gagccacatc gctgagacac 60  
catggggaag gtgaaggctg gagtcaacgg atttgggtcgt attgggcgcc tggtcaccag 120  
ggctgctttt aactctggta aagtggata t tgttgccatc aatgaccctt tcattgacct 180  
caactacatg gtttacatgt tccaatatga ttccacccat gggcaaattc catgggcacc 240  
gtcaaggctg agaacgggaa gcttgtcatc aatgggaaat cccattcacc atcttccagg 300  
gagcgagatc cctccaaaat tcaagtgggg ggcgatgctg ggcgcttgag ttacgttcgt 360  
gggagttcca ctgggccttc tttaaccac ctttgagaa gggtttggg gttcatttn 420  
caaggggggg gagcccaan ggtcttcat tttttggcc cctttt 467

&lt;210&gt; 168

&lt;211&gt; 316

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(316)

&lt;223&gt; 3' terminal sequence. desmin (DES) gene.

&lt;400&gt; 168

ggcttggtgt tnttntctct ttattgtttc tctccagagc ccctgcagca ggggagggga 60  
gggcgtgggg aggtgggcgc ccctccacc agcctgagac cgctctctgc ctctctctc 120  
tctctcttc tccagcatct cac ccacttt ctctcttct naatctctg ctccacctc 180  
cagcaccttc ggggattccc tctgtagcc cctgctttct aagtcaccc ggggctgggg 240  
aaaggaaagt aagagaccac ggggacaatt tcaagcccc cagntccac aggggctagt 300  
ccctgggnt acctgc 316

&lt;210&gt; 169

&lt;211&gt; 440

&lt;212&gt; DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(440)

<223> 5' terminal sequence. desmin (DES) gene.

<400> 169

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gttctgaggt ccataccaag aagacggtga tgatcaagac catcgagaca cgggatgggg 120
aggctcgtcag tgaggccaca cagcagcagc atgaagtgt ctaaagacag agaccctctg 180
ccaccagaga ccgtcctcac ccctgtctc actgtccct gaagccagcc ttcttccatc 240
ccagggaacac cacaccca gc cttcagtct ccccttcaca gctctggac cctcctcac 300
tgggccattc cctcgtggtt cccaacagc ggacataggc ccatccttgc tgggttcaca 360
ggggcatggc cccgggccac ttnttgcggg aacccagtt gttgaggctt tgggtgtttg 420
ggcagttgag ttgaggcttt                                     440
```

<210> 170

<211> 2218

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(2218)

<223> desmin (DES) gene.

<400> 170

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cctcgccgca tccactctcc ggccggccgc ctgccgcgcg cctcctcc gt ggcggccgca 60
gcctcgcccg cgcgctcacc atgagccagg cctactcgtc cagccagcgc gtgtcctcct 120
accgccgcac cttcgggcggc gccccgggct tcccgcctcg ctccccgctg agctcgcccg 180
tgttcccgcg ggcgggtttc ggctctaagg gctcctccag ctcggtgacg tcccgcggtg 240
accaggtgtc ggcacgctcg ggccggg cgg ggggcctggg gtcgctgcgg gccagccggc 300
tggggaccac ccgcacgccc tcctcctacg gcgcaggcga gctgctggac ttctcactgg 360
ccgacggcgt gaaccaggag ttctgacca cgcgcaccaa cgagaagggt gagctgcagg 420
agctcaatga ccgcttcgcc aactacatcg agaagggtcg cttcctggag cagcagaacg 480
cgctcgccgc cgaagtgaac cggtcaagg gccgcgagcc gacgcgagtg gccgagctct 540
acgaggagga gctgcgggag ctgcggcgcc aggtggaggt gctcactaac cagcgcgcgc 600
gcgtcgacgt cgagcgcgac aacctgctcg acgacctgca gcggctcaag gccagctgc 660
aggaggagat tcagttgaag gaagaagcag agaacaattt ggctgcc ttc cgagcggacg 720
tgatgcagc tactctagct cgcattgacc tggagcgcag aattgaatct ctcaacgagg 780
agatcgcggt ccttaagaaa gtgcatgaag aggagatccg tgagttgcag gctcagcttc 840
aggaacagca ggtccaggtg gagatggaca tgtctaagcc agacctcact gccgccctca 900
gggatatccg ggctcagtat gagac catcg cggctaagaa catttctgaa gctgaggagt 960
ggtacaagtc gaaggtgtca gacctgacct aggcagccaa caagaacaac gacgccctgc 1020
gccaggccaa gcaggagatg atggaatacc gacaccagat ccagtcctac acctgcgaga 1080
ttgacgccct caagggcact aacgattccc tgatgaggca gatgcgggaa ttggaggacc 1140
gatttgccag tgaggccagt ggctaccagg acaacattgc gcgcctggag gaagaaatcc 1200
ggcactcaa ggatgagatg gcccgccatc tgcgcgagta ccaggacctg ctcaacgtga 1260
agatggccct ggatgtggag attgccacct accggaagct gctggaggga gaggagagcc 1320
ggatcaatct ccccatccag acctactctg cctcaactt ccgagaaacc agccttgagc 1380
aaaggggttc tgagggtccat accaagaaga cggatgatgat caagaccatc gagacacggg 1440
atggggaggt cgtcagtgag gcgacacagc agcagcatga agtgctctaa agacgagaga 1500
ccctctgcca ccagagaccg tcctcaccct tgtcctcact gctccctgaa gcccagcctt 1560
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112/292

cttccatccc agga caccac acccagcctc agtcctcccg tcacagcctc tgaccctcc 1620  
tactggcca tccctcgtgg tccccaacag cgacatagcc catccctgcc tggtcacagg 1680  
catgccccgg ccacctctgc ggaccccagc tgtgagcctt ggctgttggc agtgagttag 1740  
cctggctctt gtgtggatg gagcccaggc gggagcgggtg gccctgtccc tcc cacctct 1800  
gtgacctgag gcctacgctt tggtcttga gatagcccca gagcagggtg ttgggatact 1860  
gcagggccag gactgagccc cgcagacctc cccagcccct agcccaggag agagaaagcc 1920  
aggcaggtag cctgggggac tagccctgtg gagactgggg ggcttgaat tgtccccgtg 1980  
gtctcttact ttctttccc cagcccag gg tggacttaga aagcaggggc tacaagaggg 2040  
aatccccgaa ggtgctggag gtgggagcag gagattgaga aggagagaaa gtgggtgaga 2100  
tgctggagaa gagagaggag gagagaggca gagagcggtc tgaggctggt gggaggggag 2160  
cccacctccc cagccctcc cccccctgc tgcaggggct ctggagagaa acaataaa 2218

&lt;210&gt; 171

&lt;211&gt; 367

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(367)

&lt;223&gt; 5' terminal sequence. casein kinase 2, beta polypeptide (CSNK2B) gene.

&lt;400&gt; 171

gatccacgcc cgctacatcc ttaccaacgg tggcatcgcc agatgttga aaagtaccag 60  
caaggagact ttggttactg tccctcgtgt tactgtgaga accagccaat gcttcccatt 120  
ggcctttcag acatcccagg tgaagccatg gtgaagctct actgcccga gtgcatggat 180  
gtgtacacac ccaagtcac aagacacat caccagcatg ggccgctac t ttccgactg 240  
gtttccctca catgctcttc atgggtgcat cccaggtacc ggcccagggt gaccttgcca 300  
accagttgtg gccagggtt ttacggtttt caaggttcca tncggtgggg cttaccagggt 360  
tgcaggt 367

&lt;210&gt; 172

&lt;211&gt; 1128

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1128)

&lt;223&gt; casein kinase 2, beta polypeptide (CSNK2B) gene.

&lt;400&gt; 172

gcttctcggt gtgccccgcc cgcaagcgcc ctctccggg ccttc gtgac agccagggtg 60  
tgcgcgggtc atcctgggat tggtagttcg ctttctctca tttagccagt ttctttctct 120  
accggggact ccgtgtcccg gcctccaccg cggcacctga cccttgccg ttgcgtgttg 180  
ccctctccc caccctccct aatttccact cccccacc cacttcgcct gccgcggtg 240  
ggtccgcggc ctgcgtgta gcgg tcgccc ccgttccctg gaagtagcaa cttccctacc 300  
ccacccagc cctgggtccc gtccagccgc tgacgtgaag atgagcagct cagaggagg 360  
gtcctggatt tccgtgttct gtgggtccg tggcaatgaa ttcttctgtg aagtggatga 420  
agactacatc caggacaaat ttaattctac tggactcaat gagcagggtc ctcactatcg 480  
acaagctcta gacatgatct tggacctgga gcctgatgaa gaactggaag acaaccccaa 540

113/292

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ccagagtgc ctgattgagc aggcagccga gatgctttat ggattgatcc acgcccgccta 600
catccttacc aaccgtggca tcgcccagat gttggaaaag taccagcaag gagactttgg 660
ttactgtcct cgtgtgtact gtgagaacca gccaatgctt ccca ttggcc tticagacat 720
cccagtgtaa gccatggtga agctctactg cccaagtgc atggatgtgt acacacccaa 780
gtcatcaaga caccatcaca cggatggcgc ctacttcggc actggtttcc ctacatgct 840
cttcattggt catcccgagt accggcccaa gagacctgcc aaccagtttg tgcccaggct 900
ctacggtttc aagatccatc cg atggccta ccagctgcag ctccaagccg ccagcaactt 960
caagagccca gtcaagacga ttctgtgatt ccctccccc cctgtcctgc agtctttgtc 1020
ttttcctttc ttttttgcca ccctttcagg aacctgtat ggtttttagt ttaaattaaa 1080
ggagtcgtta tcgtggtggg aatatgaaat aaagtagaag aaaaggcc 11 28
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&lt;210&gt; 173

&lt;211&gt; 475

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(475)

<223> 3' terminal sequence. golgi apparatus  
protein 1 (GLG1) gene.

&lt;400&gt; 173

```
gggttttttt ctnaaaaaaa cctttgagtt gcaggtcagg tnagttgggt ctggaagtac 60
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ntacaaactg gggcactggg atagggtagt tcctttgggn ggggtcaaggt gggctctacc 360
ccgtccnttg agctctngtg tncactncgc ttgggggatc cctccca cttcagggc 420
cantcaggna caattttacc aggtgntccc a ctgttcac agggggattt aagtt 475
```

&lt;210&gt; 174

&lt;211&gt; 483

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(483)

<223> 5' terminal sequence. golgi apparatus  
protein 1 (GLG1) gene.

&lt;400&gt; 174

```
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gctgcactgc tcagacgaga tctocagtct atgtgctgaa gaagcagcag cccaagagca 180
gacaggtcag gtggaggagt gcc tcaaggc caacctgctc aagatcaaaa cagaattgtg 240
taaatnggaa gtgctaaaca tgctgaagga aagcaaagca gacatctttg ttgacccggg 300
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cgcgggcggt caaattgttc ctgtnttcat ggggaaggcac tgggagggtt aaggcgggtt 420
gaggtttaca gcccagattg caaaaaggcg cttcattgac ccggtttgag gtgttggatt 480
ttt 483
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<210> 175  
<211> 3909  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(3909)  
<223> golgi apparatus protein 1 (GLG1) gene.

<400> 175  
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ccagggcgct ccacagccag ggccagggtc ccggggccaa ctttgtgtcc ttcgtagggc 180  
aggccggagg cggcgcccg gcgggtcagc agctgcccc gctgcctcag tcatcgagc 240  
ttcagcagca acagcagcag cagcaacagc aacagcagcc tcagccgccg cagccgcctt 300  
tcccggcggg tgggcctccg cggcggggag gagcgggggc tgggggggc tggaag ctgg 360  
cggaggaaga gtcctgcagg gaggacgtga cccgcgtgtg ccctaagcac acctggagca 420  
acaacctggc ggtgctcgag tgctgcagg atgtgaggga gcctgaaaat gaaatttctt 480  
cagactgcaa tcatttgttg tggaattata agctgaacct aactacagat cccaaatttg 540  
aatctgtggc cagagagggt tgcaaatcta ctat aacaga gattaaagaa tgtgctgatg 600  
aaccggttgg aaaaggttac atggtttcct gcttagtgga tcaccgaggc aacatcactg 660  
agtatcagtg tcaccagtac attaccaaga tgacggccat ctttttagt gattaccgtt 720  
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atthtgcctg ccgagatgat cgggagcgtt tttgtgaaaa tacacaagct ggtg agggca 1020  
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tgagagctg tgagccata attcagacat tctgccacga tgcggataac cagatagact 2160  
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tgccctttgtt tggcaaacct gggtttacct gcctgtagac aagtct ctct cataccaaca 3840
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aaaccacca 3909
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<210> 176

<211> 390

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(390)

<223> 5' terminal sequence. endothelin receptor  
type b (EDNRB) gene.

<400> 176

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tttgaatctg tcattcacat accctgtgaa gac aatacta tctacaattt tttcaggatt 120
attaaaatct tcttctttca ctatcgtagc ttaaaactctg tttggttttg tcatctgtaa 180
atacttacct acatacactg catgtagatg attaaatgag ggcaggccct gtgctcatag 240
ctttacgatg gagagatgcc agtgacctca taataaagac tgtggaactg cctgggtgca 300
gtgtccacat gacaaagggg caggtaggca ccctctcttc acccatgctg tgggttaa 360
gggtttctag gcatatgtat tatggctatt 390
```

<210> 177

<211> 4286

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(4286)

<223> endothelin receptor type b (EDNRB) gene.

<400> 177

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 aggatcaaca cagtggctga ac actgggaa ggaactggta cttggagtct ggacatctga 180  
 aacttggctc tgaaactgcg cagcggccac cggacgcctt ctggagcagg tagcagcatg 240  
 cagccgcctc caagtctgtg cggacgcgcc ctggttgccg tggttcttgc ctgcccctg 300  
 tcgcggatct ggggagagga gagaggctt ccgcctgaca gggccactcc gcttttgcaa 360  
 accgcagaga taatgacgcc accactaag accttatggc ccaagggttc caacgccagt 420  
 ctggcggcgt cgttggcacc tgcggagggt cctaaaggag acaggacggc aggatctccg 480  
 ccacgcacca tctccctcc cccgtgccaa ggacccatcg agatcaagga gactttcaaa 540  
 tacatcaaca cggttgtgtc ctgccttgtg ttcgtgctgg gg atcatcgg gaactccaca 600  
 cttctgagaa ttatctacaa gaacaagtgc atgcgaaacg gtcccaatat cttgatcgcc 660  
 agcttggctc tgggagacct gctgcacatc gtcatcgaca tccctatcaa tgtctacaag 720  
 ctgctggcag aggactggcc atttggagct gagatgtgta agctgggtgcc tttcatacag 780  
 aaagcctccg tgggaatcac tgtgctgagt ctatgtgctc tgagtattga cagatatcga 840  
 gctgttgcct cttggagtag aattaaagga attggggttc caaaatggac agcagtagaa 900  
 attgttttga tttgggtggt ctctgtgggt ctggctgtcc ctgaagccat aggttttgat 960  
 ataattacga tggactacaa aggaagttat ctgcgaatct gcttgcctca tcccgttcag 10 20  
 aagacagctt tcatgcagtt ttacaagaca gcaaaagatt ggtggctgtt cagtttctat 1080  
 ttctgcttgc cattggccat cactgcattt ttttatacac taatgacctg tgaaatgttg 1140  
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 gccaaaaccc tcttttgcct ggtccttgtc ttggccc tct gctggcttcc ccttcacctc 1260  
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 ttacggcatg gaaagaaaat cagtgggaat taagaaagcc tcgtcgtgaa agcacttaat 1800  
 tttttacagt tagcacttca acatagctct taacaacttc caggatattc acacaacact 1860  
 taggcttaaa aatgagctca ctacg aattt ctattctttc taaaaagaga tttattttta 1920  
 aatcaatggg actctgatat aaaggaagaa taagtcactg taaaacagaa cttttaaatg 1980  
 aagcttaaat tactcaattt aaaaattttaa aatcctttaa aacaactttt caattaatat 2040  
 tatcaacta ttatcagatt gtaattagat gcaaatgaga gagcagttta gttgttgcat 2100  
 ttttcggaca ctggaacat ttaaatgata aggagggagt aacagaaaga gcaaggctgt 2160  
 ttttgaagaat cattacactt tcaactagaag cccaaacctc agcattctgc aatatgtaac 2220  
 caacatgtca caaacaagca gcatgtaaca gactggcaca tgtgccagct gaatttaaaa 2280  
 tataatactt ttaaaaagaa aattattaca tcccttaca t tcagttaaga tcaaacctca 2340  
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 ctgcatgtag atg attaaat gagggcaggg cctgtgctca tagctttacg atggagagat 2580  
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 gcaggtagca cctctctca cccatgctgt ggttaaaatg gtttctagca tatgtataat 2700  
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 cgtcacatca atgcaaaagg tccgtatttt gtccagcaa aacacagtgc aatgttctca 3120  
 gagtgaactt cgaaataaat tgggcccagg agctttaact cggctctaaa atatgcccaa 3180  
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 ttgttttctg tcaaatattga atgtgatggg acagtaaacc aaaacccaac aatgtggcca 3300  
 gaaagaaaga gcaataataa ttaattcaca cccatattgg attctattta taaatcacc 3360  
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 cattttagac tctcaatttt aaattaattt tgaatcacta atattttcac agtttattaa 3480  
 tatatttaat ttctatttaa atttttagatt atttttatta ccatgtactg aatttttaca 3540  
 tcttgatacc ctttcttct ccattgtcag atcatgttct ctaattatct tgccaaattt 3600  
 tgaaactaca caciaa aagc atacttgcatt tatttataat aaaattgcat tcagtggctt 3660

117/292

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tttaaaaaaa atgtttgatt caaaacttta acatactgat aagtaagaaa caattataat 3720
ttctttacat actcaaaacc aagatagaaa aaggtgctat cgttcaactt caaaacatgt 3780
ttcctagtat taaggacttt aatatagcaa cagacaaaat tattgttaac atgg atgta 3840
cagctcaaaa gatttataaa agattttaac ctattttctc ccttattatc cactgctaata 3900
gtggatgtat gttcaaacac ctttttagtat tgatagctta catatggcca aaggaatata 3960
gtttatagca aaacatgggt atgctgtagc taactttata aaagtgtaat ataacaatgt 4020
aaaaaattat atatctggga ggatttttt g gttgcctaaa gtggctatag ttactgattt 4080
tttattatgt aagcaaaacc aataaaaatt taagtttttt taacaactac cttattttttc 4140
actgtacaga cactaattca ttaaatacta attgattgtt taaaagaaat ataaatgtga 4200
caagtggaca ttatttatgt taaatataca attatcaagc aagtatgaag ttattcaatt 4260
aaaatgccac atttctgggc tctggg                                     4286

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&lt;210&gt; 178

&lt;211&gt; 462

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(462)

<223> 3' terminal sequence. gran zyme b (granzyme  
2, cytotoxic t-lymphocyte-associated serine  
esterase 1) (GZMB) gene.

&lt;400&gt; 178

```

acancagaga tccatttatt acagtcctgc aaccccgact gccacccct tgggaattct 60
tgccctctgc ccagagatgg tcaggcccag aggaagggtta gtctcatgcc tgctgttaga 120
ggcgnttcat tgttctcttt atccagggca ggaagtntga gaccttgatg tagactcctg 180
ggggtgtccc tttttgttt ccataggaga gaataccttg ggctangtcc ttacananga 240
ggggcccccc ggagttcccc cttgaaaccg gtctgtgtct tctttggatc cccacacaa 300
atntcagtgg gctctgctgt aattgccatg ggaaggagac gggtcac ant gggcagttcc 360
ttctgcactn ttcaggaaca atttctgaa gtgtgggttg ctaaagtgtc cattgagaaa 420
taaccccgag ccaggccaaa ttgaaaagtt gcctgggntt tt                                     462

```

&lt;210&gt; 179

&lt;211&gt; 960

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(960)

<223> granzyme b (granzyme 2, cytotoxic  
t-lymphocyte-associated serine esterase 1) (GZMB)  
gene.

&lt;400&gt; 179

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agcagctcca accagggcag ctttctgag aagatgcaac caatcctgct tctgtctggcc 60
ttctctctgc tgcccagggc agatgcaggg gagatcatcg ggggacatga ggccaagccc 120
cactcccgcc cctacatggc ttatcttatg atctgggatc agaagtctct gaagaggtgc 180
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ataaatgtca ctttgggggc ccacaatatc aaagaacagg agcc gaccca gcagtttatc 300
cctgtgaaaa gaccatccc ccatccagcc tataatccta agaacttctc caacgacatc 360

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118/292

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acggccccc tgggaaaaca ct cacacaca ctacaagagg tgaagatgac agtgcaggaa 540  
gatcgaaagt gcgaatctga cttacgcoat tattacgaca gtaccattga gttgtgcgtg 600  
ggggaccag agattaaaaa gacttccttt aagggggact ctggaggccc tcttgtgtgt 660  
aacaaggtgg cccagggcat tgtctcctat ggacgaaaca atggcatgcc tccacgagcc 720  
tgcaccaaag tctcaagctt tgtactctgg ataaagaaaa ccatgaaacg ctactaacta 780  
caggaagcaa actaagcccc cgctgtaatg aaacaccttc tctggagcca agtccagatt 840  
tacctggga gaggtgccag caactgaata aatacctctc ccagtgtaaa tctggagcca 900  
agtccagatt tactctggga gaggtgccag caactgaata aa tacctctt agctgagtgg 960

&lt;210&gt; 180

&lt;211&gt; 471

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(471)

<223> 3' terminal sequence. fibroblast growth  
factor receptor 1 (fms-related tyrosine kinase 2;  
pfeiffer syndrome) (FGFR1) gene.

&lt;400&gt; 180

tnaagcagca gcaattttta ttgagggacc taaactgaaa ataggtttag aacataattt 60  
aaaaaaataa aacagcaaaa gtagcaaaaa atatatgacc tttttaaaaa cattttcctt 120  
ttttttcttt ttgtttttta atatatagca actga tgcct cccagccacc agngcatct 180  
taccgatgg gtaaatctct ggtaacgacc cttttaaaaa gacatgtaaa tatatactca 240  
gntttataca ctttgtgttt tcttcatagc tatntacaga gccccagtt tgggctgggc 300  
caggggcan caacactgcc cccaacctgg gccttcgct caccatctc tgggtaccgg 360  
gcntttgggt caggcaaaagc aaactagtnt cgggtttatt angccactgg naccaccttt 420  
ttgggggcag aggtcacctt cattcgaggg cacgangcac tgacctcctt t 471

&lt;210&gt; 181

&lt;211&gt; 463

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(463)

<223> 5' terminal sequence. fibroblast growth  
factor receptor 1 (fms-related tyrosine kinase 2,  
pfeiffer syndrome) (FGFR1) gene.

&lt;400&gt; 181

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gagctttctc ctgtcggttt ggtctgttt gccttcaccc ataagcccct cgactntgg 180  
tggcaggtgc cttgtcctca gggctacagc agtagggagg tcagtgtctc gtgcctcgat 240  
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cagtgttggt gccngggggc agcccaaaac tgggggcttc tgtatatagc tattgaagaa 420

aacacaaatg tattaatctg agtatatatt ttacatgtnt ttt

463

&lt;210&gt; 182

&lt;211&gt; 4066

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(4066)

&lt;223&gt; fibroblast growth factor receptor 1

(fms-related tyrosine kinase 2, pfeiffer syndrome)

(FGFR1) gene.

&lt;400&gt; 182

cctcttgcgc ccacaggcgc ggcgtcctcg gggcgggcg gcagctagcg ggagccggga 60  
cgccggtgca gccgcagcgc gcggaggaac cggggtgtgc cgggagctgg gcggccacgt 120  
ccggacggga ccgagacccc tcgtagcgca ttgcggcgac ctgccttcc ccggccgcga 180  
gcgcgcgct gcttgaaaag ccgcggaacc caa ggacttt tctccggtcc gagctcgggg 240  
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gcccgggggc gccgggcccg agccggggac gcgggcacac gccgcctcgc acaagccacg 600  
gcggaacttc ccgagggcga acctccacgc cgagcgaggg tcagtttgaa aag gaggatc 660  
gagctcactg tggagtatcc atggagatgt ggagcctgt caccaacctc taactgcaga 720  
actgggatgt ggagctgaa gtgcctctc ttctgggctg tgctggtcac agccacactc 780  
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&lt;210&gt; 183

&lt;211&gt; 415

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(415)

<223> 5' terminal sequence. protein phosphatase 2  
(formerly 2a), catalytic subunit, alpha isoform  
(PPP2CA) gene.

&lt;400&gt; 183

```

cagttatatc cctccatcac tagctggtga gctctagaca ccaacgtgag gccattggat 60
tgattaaatg tctcagaaat atcttgccca aagggtgaac cagctcctcg aggagatata 120
ccccaaccac cagggtcatc tggatctgac cacagcaagt cacacattgg accctcatgg 180
ggaacttctt gtaggcgacg aagtgcctctg atatgatcca gtgtat ctat agatggcgag 240
agaccacatg gttagcagaa gatctgccc tccaccaagg cagtgaaggg aagatagtca 300
aaaagatctg taaaatattt ccaaacattt ggcatttcca tattttctta aacattcatt 360
ctaggaaacc ttaacttgt gtgnatctgt cnggtcttct ggtttccctg gagga 415

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&lt;210&gt; 184

&lt;211&gt; 2181

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

121/292

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2181)

<223> protein phosphatase 2 (formerly 2a),  
catalytic subunit, alpha isoform (PPP2CA) gene.

&lt;400&gt; 184

```
agagagccga gctctggagc ctacgagcgg ggaggaggag gcgcagggcc gacggccgag 60
tactgcggtg agagccagcg ggccagcgcc agcctcaaca gcgcagagaa gtacacgagg 120
aaccgcgcg cgcgtgtgct ttagggcccg tctgcgggcg gcggcgcggg aggagcgagg 180
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tctgcgagaa ggctaaagaa atcctgacaa aagaatccaa cgtgcaagag gttcgatgtc 360
cagttactgt ctgtggagat gtgcatgggc aatttcatga tctcatggaa ctgtttagaa 420
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actatcttcc tctcactgcc ttggtggatg ggcagatctt ctgtctacat ggtggctctt 720
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agacttaatt gtaaaaccaa ataacttgag atttaagtct ttgggttggt ttttaataaa 2160
acagcatggt ttcaggtaga g                                     2181
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&lt;210&gt; 185

&lt;211&gt; 375

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(375)

<223> 5' terminal sequence. homo sapiens, clone  
image:4054156, mrna, partial cds (EST R55460)  
gene.

122/292

&lt;400&gt; 185

cgaagaggat gaggaagagc tncgtgtgct gcancaagag ctccaggccg ggctgcgcac 60  
caaggccctg attgtggatg agtcctgccg gcggnacca tcttccaaca tagggatata 120  
cctccctcct tcttataact gaagatcctg gagcccgaa gattcag ggc agacagaccc 180  
tgataatgag cctggcaggg aagggaacc aacatcttgt aacttgctt cccaccctg 240  
tttctggggg cagagcaatt gcccaatttc taccctaate caaagtcctt ggggtgnggt 300  
ggggttaaac gtgctggtgc atcctaggtc atccaagagt gaggcgcaa gttcctgagg 360  
aagggggcac agaac 375

&lt;210&gt; 186

&lt;211&gt; 542

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(542)

<223> 3' terminal sequence. immunoglobulin kappa  
constant (IGKC) gene.

&lt;400&gt; 186

gcaaagattc acaatattta ttnattctcc tccaacatta gcataattaa agccaaggag 60  
gaggaggggg gtgaggtgaa agatgagctg gaggaccgca ataggggtag gtcccctgtg 120  
gaaaaagggt cagaggccaa aggatgggag ggggtcaggc tgganctgag gagcaggtgg 180  
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cctgatggg tgacttcgca ggcgtagact ttgtgtttct cgtagtctgc tttgctcagc 300  
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ctgggggant taccnattt gggaggcgt tatccacctt ccaactgtact ttggc ctctc 420  
tggggataga agttttttca gcaggcacac aacagaggca nttccagatt tncaactgct 480  
catcagatgg ccgggaagnt gaaggncagt nggtgcagcc acattncitt tgatccncca 540  
ct 542

&lt;210&gt; 187

&lt;211&gt; 296

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(296)

<223> 5' terminal sequence. melanocortin 1  
receptor (alpha melanocyte stimulating hormone  
receptor) (MC1R) gene.

&lt;400&gt; 187

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acatctccat cttctacgca ctgnctacca cagcatcgtg accctgccgc gggcggaag 120  
nccgttgagg ccatctgggt ggccagtgtc gtcttcagca cgctcttcat cgcctactac 180  
gaccacgtgg ccgtcctgct gtgcctcgtg gtcttcttcc tggctatgct ggtgctcatg 240  
gccgtgctgt acgtccacat gctggcccgg gcctgccagc acgccagggt cattcg 296

&lt;210&gt; 188

123/292

<211> 1270  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(1270)  
<223> melanocortin 1 receptor (alpha melanocyte  
stimulating hormone receptor) (MCLR) gene.

<400> 188  
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agtgttgaag 1270

<210> 189  
<211> 336  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(336)  
<223> 3' terminal sequence. neuregulin 1 (NRG1)  
gene.

<400> 189  
ccaanaccaa atccgagccc ttggacaaa ctgcctgcg ccgagagccg tccgcgtaga 60  
gcctccgtct ccggcgagat gtccgagcgc aaagaaggca gaggcaaagg gaagggcaag 120  
aagaaggagc gaggtcgcnc aagaagccgg ntccgggggc ggngcagcag gagcccagcc 180  
ttgcctcccc aattnaaaga gatgaaaagc caggaatcgg ctgcaggttc caaactagtc 240  
cttcggtgtg aaaccagttc tgaatactcc tctctcagat tcaagtgggt caagaatggg 300  
gaatgaattg aatcgaaaaa nncannccac aaaatt 336

124/292

<210> 190  
<211> 366  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(366)  
<223> 5' terminal sequence. neuregulin 1 (NRG1)  
gene.

<400> 190  
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cattctcggg gggtnngtta ggatggtag gcccattggc aatgttcac atattgtttc 120  
gttcagaccg aagctctgcc agagacggtc atgcagcttt ttccgctgtt tcttggtttt 180  
gcagtaggcc accacacaca tgatgccgac cacaaggagg gcgatgcaga tgccggttat 240  
ggtcagact ctcttctggt acagctcctn cgctncata aattcaatnc caagatgctt 300  
gtagaagctg gccattnacg tagttttttg gcagcgattc accagtaaaa cttcatttng 360  
gggcac 366

<210> 191  
<211> 2490  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(2490)  
<223> neuregulin 1 (NRG1) gene.

<400> 191  
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caggacggtg ataactctc cccgatcggg ttgcgagggc gccgggcaga ggccaggacg 180  
cgagccgccca gcggcgggac ccacgcagca cttcccgggg cgacaggagc agccccgaga 240  
gccagggcga gcgcccgttc caggtggccg gaccgcccgc cgcgtccgag ccgcgctccc 300  
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cccatcgagg gacaaacttt tcccaaaccg gatccgagcc cttggacca actcgcctgc 420  
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attcaagtgg ttcaagaatg ggaatgaatt gaatcgaata aacaaaccac aaaatatcaa 720  
gatacaaaaa aagccaggga agtcag aact tcgcattaac aaagcatcac tggctgattc 780  
tgagagatg atgtgcaaag tgatcagcaa attaggaaat gacagtgcct ctgccaatat 840  
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atctacatct acatccacca ctgggacaag ccattctgta aatgtgagg agaaggagaa 1020  
aactttctgt gtgagtgagg gggagtgcct catggtgaaa gacctttcaa acccctcgag 1080  
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gcggaaaaag ctgcatgacc gtcttcggca gagccttcgg tctgaacgaa acaatatgat 1320  
gaacattgcc aatgggcctc accatcctaa cccaccccc gagaatgtcc agctggtgaa 1380

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tcaatacgta tctaaaaa cg tcatctccag tgagcatatt gttgagagag aagcagagac 1440
atcctttttcc accagtcact atactttccac agcccatcac tccactactg tcaccagac 1500
tcctagccac agctggagca acggacacac tgaaagcatc ctttccgaaa gccactctgt 1560
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cagcctccct gctagccct tgaggatagt ggaggatgag gagtatgaaa cgaccaaga 2040
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&lt;210&gt; 192

&lt;211&gt; 453

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(453)

&lt;223&gt; 5' terminal sequence. ciliary neurotrophic factor receptor (CNTFR) gene.

&lt;400&gt; 192

```

cagatgctac gccgggaagg agtacattat ccagggtggca gccaaaggaca atnagattgg 60
gacatggagt gactggagcg taccgcccac gctacgccct ggactgagga accgcgacac 120
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agtctcttga tctgagcccg gcaccccatg aggacatgca gagcacctgc agaggancag 360
gaggccggag cttgagcctt gtagaccccg gtttctattt t ncacacggg caggaggant 420
ttttgcattn tttttnagac acaatttttt gga 453

```

&lt;210&gt; 193

&lt;211&gt; 1566

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1566)

&lt;223&gt; ciliary neurotrophic factor receptor (CNTFR) gene.

&lt;400&gt; 193

126/292

```

gcggcgccag cggaggcgcc ggctccagcc ggcgccggcg gaggctcgcc ggtgggatcc 60
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gcggcgccgaa gcccgggtgg cccgagggcg cgaactct agc cttgtcacct catcttgccc 180
ccttggtttt ggaagtccctg aagagttggt ctggaggagg agggagacat tgatgtgctt 240
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caagct 1566

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&lt;210&gt; 194

&lt;211&gt; 349

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(349)

<223> 5' terminal sequence. angiogenin,  
ribonuclease, rnase a family, 5 (ANG) gene.

&lt;400&gt; 194

```

ccgtgtacac acactcacac aaggacgcca accccaccta gatgcaaaga ggattcaaaa 60
gaacatcttt gcgttttcta ccggtccccc atcatcgtag tagggaggaa gaagcggtg 120
agaaacaaaa cttctttcca ttgtcctgcc cgtttctgcg gacttggtct gaggccgagg 180
agcctgtggt ggaagagatg gtgatgggcc tgggcgtttt gttgttggtc ttcgtgctgg 240
gtctgggtct gacccaccg acctggctc aggataactn c aggtacaca cacttctga 300
cccagcacta tgatgccaaa ccacagggcc ngggatgaca gatactgtg 349

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&lt;210&gt; 195

&lt;211&gt; 729

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

<221> misc\_feature  
<222> (1)..(729)  
<223> angiogenin, ribonuclease, rnase a family, 5  
(ANG) gene.

<400> 195  
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gggcccggat gacagatact gtgaaagcat catgaggaga cggggcctga cctcaccctg 300  
caaagacatc aacacattta ttcattggca caagcgcagc atcaaggcca tctgtgaaaa 360  
caagaatgga aaacctcaca gagaaaacct aagaataagc aagtcttctt tccagggtcac 420  
cacttgcaag ctacatggag gttcccctg gcctccatgc cagtaccgag ccacagcggg 480  
gttcagaaac gttgtgtgtg cttgtgaaaa tggcttaoct gtccacttgg atcagtcaat 540  
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ccatttcccc tctgcacca gaacagtgtt ggcaacattc attgccaagg gcccaaagaa 660  
agagctacct ggaccttttg ttttctgttt gacaacatgt ttaataaata aaaatgtctt 720  
gatatcagt 729

<210> 196  
<211> 452  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(452)  
<223> 3' terminal sequence. endoglin  
(osler-rendu-weber syndrome 1) (ENG) gene.

<400> 196  
ngttactcca gccttggacc ggggctgcca ctt ggagagn cgtggcgacc acaaggaggc 60  
gcacatcctg agggctcctg cgggccactc ggcgggcccc ggacgggtga cgggtgaagg 120  
ggaactgagc tgcgcacccg gggatctcga tgcctctctc atcctgcagg gtcccccta 180  
cgtgtcctgg ctcatcgagc ccaaccacaa catgcagatc tggaccactg gagaatactc 240  
cttcaagatc tttccagaga aaaacattcg tggcttcaag ctcccagaca cacctcaagg 300  
cctcctgggg ggacgcgngn atgcttcaat gccagcattg tggcatcctt cgtgggagct 360  
taccgctggg ccagcattgt cttnatattc ttgccttcca gcttgcggtt gttagggttg 420  
cagaccttaa cccgnaccgt ttccagacca tt 452

<210> 197  
<211> 379  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(379)  
<223> 5' terminal sequence. endoglin  
(osler-rendu-weber syndrome 1) (ENG) gene.

<400> 197



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aggacgagc ctttgcttgt gcaaccagac aggtcagggc tgatgatgtt caagcgcatg 60  
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agctgagggt gccggttttg ggtatgggta ctgtgtagaa gtggaggagg aagctgaagc 180  
gcgggtcacc ctcggggctt ggggacagca ggct cacaca gttgcccttg gccgcccggc 240  
cctgggatga gttccacggg gcctccctca ggccccaagt ccagggtggc agctgtctaa 300  
ctggagcagg aactcggaga cggatgggga cantctgacc tgcacaaagc tttntttgcc 360  
ccggcttcga tgggtgtttt 379

&lt;210&gt; 198

&lt;211&gt; 3142

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(3142)

<223> endoglin (osler-rendu-weber syndrome 1)  
(ENG) gene.

&lt;400&gt; 198

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catctgcgcc ctggggccag gactgctgct gtcactgcca tccattggag ccagcaccc 120  
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gcaogtcccc tctggctgtt gccctgctgc tggccagctg cagcctcagc cccacaagtc 420  
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gcaaaggcct cgtcctgccc gccgtgctgg gcatcacctt tgggtgccttc ctcatcgggg 2160  
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gcaccaacca cagcatcggg a gcaccaga gcacccctg ctccaccagc agcatggcat 2460
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&lt;210&gt; 199

&lt;211&gt; 402

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(402)

<223> 3' terminal sequence. epidermal growth  
factor (beta-urogastrone) (EGF) gene.

&lt;400&gt; 199

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tatgtttttg gtgattttat ttaataaatt agaagaaatt catcgttgct tataatgaaa 60
acaaatcagg caatttactt acaatcttgt aactgaaaat acatacaaa t tctgtgcaat 120
cacaccaaga gggaaaattc tgtaggggaa aaggacagta atgactaaga aactccgaag 180
cctcctgtgt aatattttta aaataaaatg ttttcattca aatattttta aaaataagcc 240
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aacggtattg taatattcca atcatttcat gaaactgata ta 402
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&lt;210&gt; 200

&lt;211&gt; 4877

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(4877)

<223> epidermal growth factor (beta-urogastrone)  
(EGF) gene.

&lt;400&gt; 200

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agctggaact ttccatcagt tcttctttc ttttctctct ctaagccttt gccttgctct 120
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 agtggctggg gaggatggc aggcagcaga tgggtcaatg caaccaactt catggaggca 3840  
 ggagccccag ttatgtggaa tgggcacaga gcaaggctgc tggattccag tatccagtga 3900

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```

taagggtcc tgtccccagg taatggagcg aagctttcat atgccctcct atgggacaca 3960
gacccttgaa gggggtgtcg agaagcccca ttctctccta tcagctaacc cattatggca 4020
acaaagggcc ctggaccac cacac caaat ggagctgact cagtgaaaac tggattaaa 4080
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acagatacgt agttgtgctt ttgtttgctc ttttaagcag tctcactgca gtcttatttc 4260
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aaaatcacca aaaacat
4877

```

<210> 201  
 <211> 153  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(153)  
 <223> 3' terminal sequence. hmt1 (hnrnp  
 methyltransferase, s. cerevisiae) -like 1 (HRMT1L1)  
 gene.

```

<400> 201
attagacctc acattagggg aaacatcaaa atgantcacg cagcaccctt gagatcctga 60
ggttggccca gccgagcccg tgctcagaag cccccagct cgggccccca gctgcccgca 120
cgcccgccct caccagcagg caggtcccca tcc
153

```

<210> 202  
 <211> 472  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(472)  
 <223> 5' terminal sequence. hmt1 (hnrnp  
 methyltransferase, s. cerevisiae) -like 1 (HRMT1L1)  
 gene.

```

<400> 202
agtgaatcgc agggagaaga gcctgctgag tncagtgagg cgggtctcct gcaggaggga 60
gtacagccag aggagtttgt ggccatcgcg gactacgctg ccaccgatga gaccagctc 120
agttttttga gaggagaaaa aattcttatc ctgagacaaa cactgcaga ttggtggtgg 180
ggtgagcgtg cgggctgctg tgggtacatt c cggaacc atgtggggaa gcacgtggat 240
gagtacgacc ccaggacac gtggcaggat gaagagtact tcggcagcta tggaaactctg 300

```

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```

aaactccact tgggagatgt tggcagacca gccacgaaca actaaatacc acagtgttca 360
ttcctgncag gaattaaaga atccctgnac ggnttaaagt tcttcnngg acgtggggct 420
gtggggattt gggatccntc agtctctnt tgttgacat tttgcgtggc nt 472

```

&lt;210&gt; 203

&lt;211&gt; 2093

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2093)

<223> hmt1 (hnrnp methyltransferase, s.  
cerevisiae)-like 1 (HRMT1L1) gene.

&lt;400&gt; 203

```

cactgcgctt gcgcgggttg agggcggttg ctacgtctcc tggaaaggac cgtccacccc 60
tccgcgcttg cgggtgtggac gcggaactca gcgagaaac gcgattgaga aatggaaaag 120
aaaatgaaat aaatcagcag ttatgaggca gagcctaaga gaactatggc aa catcaggt 180
gactgtccca gaagtgaatc gcaggagaa gagcctgctg agtgcagtga ggccgggtctc 240
ctgcaggagg gagtacagcc agaggagttt gtggccatcg cggactacgc tgcaccgat 300
gagacccagc tcagtttttt gagaggagaa aaaattotta tcctgagaca aaccactgca 360
gattggtggt ggggtgagcg tgcgggctgc tgtgggtaca ttccggcaaa ccatgtgggg 420
aagcacgttg atgagtacga ccccgaggac acgtggcagg atgaagagta cttcggcagc 480
tatggaactc tgaactcca cttggagatg ttggcagacc agccacgaac aactaaatac 540
cacagtgtca tcctgcagaa taaagaatcc ctgacggata aagtcatect ggacgtgggc 600
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gtgccagtgg cgtgtaggga aactgccct ggctcagcgt gcgagctaag gtggcgatgt 1980
atgcgatggg actctgcatg ggatagtaca gttgtgtaga cgtcttccaa ataaattatg 2040
tgttggtgcc atcgcacatg ctcaataaat attttaaat agtgaaaaaa aaa 2093

```

&lt;210&gt; 204

&lt;211&gt; 431

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(431)

<223> 3' terminal sequence. ets variant gene 4  
(ela enhancer-binding protein, elaf) (ETV4) gene.

<400> 204

```
tgggggcctt  tatta aggtc  tggcagatgt  ggtggagggtg  gaagtacaaa  cccaggcctg  60
ggcctaggaa  agggcagaag  aaaggcaaag  ggtcccttgg  agcaggaacc  catccctctc  120
tgcttatacc  cagcaccctt  catcccaggt  tcctttcttc  aacctccgcc  tgctcttggg  180
aacacagagc  accaagaact  gacaaaccgg  gaccctccag  gggccacagc  gtgggggc  ag  240
agtccagggn  ttctgtctcc  ccgcagtggg  gagatctngg  ggagctcagg  tgaacctcct  300
cancctcctg  ccagtatgaa  gttggggaag  cgccttttct  tgtccccag  aacagaacaa  360
actcttggtc  tctgtgggtt  ngggggaaaa  ggtttngggg  ggtttggact  taggggagaa  420
gttnagcttg  a                                     431
```

<210> 205

<211> 435

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(435)

<223> 5' terminal sequence. ets variant gene 4  
(ela enhancer-binding protein, elaf) (ETV4) gene.

<400> 205

```
gtcccctgcc  cctgcccttg  gacagtgcgc  cctacagncc  tttccccggg  cagagaacgg  60
aatttcctga  gatcctcttg  cacctcccag  ccccaccctg  gccatgggta  cctcggggaa  120
catagctccg  tcttcagca  gccctggga  catttgccac  tccttcacat  ctcagggagg  180
gggcccggaa  cccctcccag  gccccctacc  aacaccagct  gtggagccc  tgcccacct  240
atccccagca  gagctttaag  caagaatacc  atgatcccct  gtatggaaca  gggngggggc  300
agccaggccg  tgggaaccag  ggtgggggt  tcaatggggg  cacagggtac  ccaggggggn  360
ggggggttg  ttgattcaaa  acagggaaca  gacgggattt  tt  ggnttaag  gatttnaggt  420
tntttaancg  gggtg                                     435
```

<210> 206

<211> 447

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(447)

<223> 5' terminal sequence. annexin a11 (ANXA11)  
gene.

<400> 206

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```

agaccccagt cctctttgac atttatgaga taaaggaagc catcaagggg gttggcactg 60
atgaagcctg cctgattgag atcctcgctt cccgcagcaa tgagcacatc cgagaattaa 120
acagagccta caaagcagaa ttcaaaaaga ccctggaaga ggcca ttcga agcgacacat 180
cagggcactt ccagcggctc ctcatctctc tctctcaggg aaaccgtgat gaaagcacia 240
acgtggacat gtactcgcc cagagagatg cccagggagc tgtatgcggn ccggggagaa 300
ccgcctgggg aacagacgag tccaagtttc aattgcggtt tctgtggctt cccgggagcc 360
gggcncacc tgggtaggca gtt tttcaat gagttaccag agaatgnaca gggcncggac 420
attntagaa gagcatctgc ccggaga 447

```

&lt;210&gt; 207

&lt;211&gt; 1958

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1958)

&lt;223&gt; annexin a11 (ANXA11) gene.

&lt;400&gt; 207

```

gctgctgcgc ccgcggctcc ccagtgcctc gagtgccccg cgggccccgc gagcgggagt 60
gggaccacgc cctaggcaga acccaggcgc cgcgcgccgg acgccccggg agagagccac 120
tcccgccac gtccatttc gccctcgcg tccggagtcc ccgtggc cag atctaaccat 180
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gacctgggtc ggtctagaac tctctcagga tgccctttct accccatccc tcacagcctc 1920
ttgctgctaa aatagatggt tcatttttct gaaaaaaa 1958

```

&lt;210&gt; 208

&lt;211&gt; 433

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(433)

<223> 5' terminal sequence. platelet-derived  
growth factor receptor, beta polypeptide (PDGFRB)  
gene.

&lt;400&gt; 208

```
gccagatgaa gcaaggccat ataccctaaa cttccatcct gggggtcagc tnggctcctg 60
ggagattcca gatcacacat cacactctgg ggactcagga accatgcccc ttcccaggc 120
ccccagcaag tctcaagaac acagctgcac aggccttgac ttagagtnac agccggtntc 180
ctggnaagcc cccagcagct gccccaggga catgggaaga ccacgggacc tctttcacta 240
cccacgatga cctccggggg tatcctgggg caaaagggac aaagagggca aatgagatca 300
cctnctgcag cccaccactt ccagcacctg tgccgaggtt ttic gttcga agacagaatt 360
ggacagttga ggacagttat tgtctttntt taaaagnaca aggaagggtt cagnttgggt 420
tacccecaag gag                                     433
```

&lt;210&gt; 209

&lt;211&gt; 5570

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(5570)

<223> platelet-derived growth factor receptor,  
beta polypeptide (PDGFRB) gene.

&lt;400&gt; 209

```
ggccccctcag ccctgctgcc cagcacgagc ctgtgctgcg cctgccccaac gcagacagcc 60
agaccacagg cgccccctct ggcggtctctg ctccctccga aggatgcttg gggagtgagg 120
cgaagtctgg cgctcctctc ccctacagca gcccccttcc tccatccctc tgttctcctg 180
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```



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 tctgtgactt tggcctggct cgaga catca tgcgggactc gaattacatc tcaaaggca 2940  
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 gcatggccca gctgcccac gctccgacg agatctatga gatcatgcag aagtgtctgg 3180  
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 tggacaccag ctccgtctc taaactgccc tgcagcccaa tgagggtgac aacgactata 3420  
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 cttgacttag agtgacagcc ggtgtcctgg aaagccccc gcagctgccc cagggacatg 4920  
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137/292

```
gggacaaaga gggcaaatga gatcacctcc tgcagccac cactccagca cctgtgccga 5040
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ttacaaatat ttttaggact cacgttaact cacatttata ca gcagaaat gctattttgt 5520
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```

&lt;210&gt; 210

&lt;211&gt; 406

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(406)

<223> 5' terminal sequence. williams-beuren  
syndrome chromosome region 14 (WBSCR14) gene.

&lt;400&gt; 210

```
gaccggcgta tcacacacat ctccgaggac aggaagcggc gcttcaacat caagctgggg 60
tttgacaccc ttcatgggct cgtgagcaca ctcaagtccc agcccagcct caaggtgagc 120
aaagctacca cgctgcagaa gacagctgag tacatcctta tgctacagca ggagcgtgcg 180
ggcttgcaagg aggaggccca gcagctgcgg ggatgagatt gaggagctca atgccgccat 240
taacctgtgc cagcagcagc tgcccggcac aggggtaccc attcacacac cagcgttttg 300
accagatgcg agacatgttt gatggactac gtccgaaccc gtacgctgca caa ctgggaa 360
gttctgggggt ntttcagcat cctnattccg gcctctgttt tgagtc 406
```

&lt;210&gt; 211

&lt;211&gt; 3293

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(3293)

<223> williams-beuren syndrome chromosome region  
14 (WBSCR14) gene.

&lt;400&gt; 211

```
ccccgcgctg cgcggagcag ggaccaggcg gttgcggcgg cgacagccat ggccggcgcg 60
ctggcaggtc tggccgcggg cttgcaggtc ccgcgggtcg cgcccagccc agactcggac 120
tcggacacag actcggagga ccgagctctc cggcgcagc g cgggcggctt gctcgcctcg 180
caggatcatc acagcgggtc cttcatggtg tcgtcgccgc acagcgactc gctgcccccg 240
cggcgcgacc aggaggggtc cgtggggccc tccgacttcg ggccgcgcag tatcgacccc 300
acactcacac gctctcttca gtgcttgagc ctggcctaca gtggcaagct ggtgtctccc 360
aagtggaaga atttcaa agg cctcaagctg ctctgcagag acaagatccg cctgaacaac 420
gccatctgga gggcctggta tatccagtat gtgaagcggg ggaagagccc cgtgtgtggc 480
ttcgtgaccc ccctgcaggg gcctgaggct gatgcgcacc ggaagccgga ggccgtggtc 540
ctggaggggg actactggaa gcggcgcacg gaggtggtga tgcgggaata ccacaagtg g 600
```

138/292

```

cgcatctact acaagaagcg gtcocgtaag cccagcaggg aagatgacct cctggcccct 660
aagcaggcgg aaggcagggt gccgcgcgcg gagcaatggt gcaaacagct cttctccagt 720
gtgggtcccc tgctgctggg ggacccagag gaggagccgg gtgggcggca gtcctggac 780
ctcaattgct tttgtccga catctcagac actctct tca ccatgactca gtccggccct 840
tcgcccctgc agctgccgccc tgaggatgcc tacgtcggca atgctgacat gatccagccg 900
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cccgtggttg actcctctt cagcagtggg accctgggccc cagaggtgcc cccggcttcc 1080
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agcagggcag gcatcatg tg tgtgtgtgtg tgtggatgtg tgtgtgtggg tttgttaaag 3240
aattcttgac caataaaagc aaaaactgtc tgctggttaa aaaaaaaaaa aaa 3293

```

&lt;210&gt; 212

&lt;211&gt; 207

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(207)

&lt;223&gt; 5' terminal sequence. cd74 antigen

(invariant polypeptide of major histocompatibility  
complex, class ii antigen-associated) (CD74) gene.

&lt;400&gt; 212

```
cctttggcct tggcttttct agtcctatct acctgtcagg ctgagccatc tctcttccc t 60
ttccccagtc atcactcccc aaggaagagc caatgttttc cacccataat cttttctgcc 120
gacccttagt tccctctgct cagccaagct tgttatcagc ttccagggcc atngttcaca 180
ttagaataaa aggtagtaat taganaa                                     207
```

&lt;210&gt; 213

&lt;211&gt; 1304

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1304)

&lt;223&gt; cd74 antigen (invariant polypeptide of major histocompatibility complex, class ii antigen-associated) (CD74) gene.

&lt;400&gt; 213

```
ttcccagatg cacaggagga gaagcaggag ctgtcgggaa gatcagaagc cagtcatgga 60
tgaccagcgc gaccttatct ccaacaatga gcaactgccc atgctggggc gccgccctgg 120
ggccccggag agcaagtga gccgcggagc cctgtacaca ggcttttcca tcctggtgac 180
tctgtctctc gctggccagg ccaccaccgc ct acttcctg taccagcagc agggccggct 240
ggacaaactg acagtcacct cccagaacct gcagctggag aacctgcgca tgaagcttcc 300
caagcctccc aagcctgtga gcaagatgag catggccacc ccgtctgctga tgcaggcgct 360
gcccatggga gccctgcccc agggggcccat gcagaatgcc accaagtatg gcaacatgac 420
agaggaccat gtgatgcacc tgctccagaa tgctgacccc ctgaagggtgt acccgccact 480
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tggtgctggg gtgaccaagc aggatctggg cccagtcccc atgtgagagc agcagaggcg 720
gtcttcaaca tcctgccagc cccacacagc tacagctttc ttgtctcctt cagccccag 780
cccccccc atgtcccacc ctgtacctca tcccatgaga cctgggtgcct ggctctttcg 840
tcacccttgt acaagacaaa ccaagtggga acagcagata acaatgcagc aaggccctgc 900
tgcccaatct ccattgtgca acaggggagc gaggtcccag gaagtggcca aaagctagac 960
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atgtctgact tcctctcccc tcagcctttt ggcttggct tttctagcct atttacctgc 1140
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ggaccataa tcctttctgc cgaccctag ttccctctgc tcagccaagc ttgttatcag 1260
ctttcagggc catggttcac attagaataa aaggtagtaa ttag                                     1304
```

&lt;210&gt; 214

&lt;211&gt; 355

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(355)

&lt;223&gt; 5' terminal sequence. annexin a7 (ANXA7) gene.

140/292

```

<400> 214
aggaactatc cgaccagctg ccaacttcga tgctataaga gatgcagaaa ttcttcgtaa 60
ggcaatgaag ggttttgga cagatgagca ggcaattgtn gatgtngttg ccaaccgttt 120
ccaatgatca gaggcaaaaa attaaagcag catttaagac ctccatggc aaggatttaa 180
tcaaagatct caaatcagag ttaagtngaa atatggaaga actgatccn ggccctcttc 240
atgcctccta cgtattacga tgcctngagc tttacggaaa gcaatncagg gancaggta 300
tcaggancgt tgtatttgat ttgngatfff ngtgcacang atcanattca ggtaa 355

```

```

<210> 215
<211> 2176
<212> DNA/RNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:primer

```

```

<220>
<221> misc_feature
<222> (1)..(2176)
<223> annexin a7 (ANXA7) gene.

```

```

<400> 215
gaacccggtc tcccgcaaga tggagccggg ttgggctgtg acgctgctgc tggggtcaga 60
atgtcatacc caggctatcc cccaacaggc taccacacct tccctggata tcctcctgca 120
ggtcaggagt catcttttcc cccttctggt cagtatccct atccatagtg ctttcctcca 180
atgggaggag gtgctaccc acaagtgcga agtagtggt acccaggagc tggaggctac 240
octgocgctg gaggttatcc agccctgga ggcctatcct gtgccccaca gccaggggga 300
gctccatcct atcccgaggt tctccaggc caaggatttg gagtcccacc agg tggagca 360
ggcttttctg ggtatccaca gccaccttca cagtcttatg gaggtgtgct agcacagggt 420
ccactacctg gtggctttcc tggaggacag atgccttctc agtatcctgg aggacaacct 480
acttaccta gtcagatcaa tacagattct ttttcttcc atcctgtttt ctctcctgtt 540
tctttggatt atagcagtga acctgccaca g tgaactcagg tcaactcaagg aactatccga 600
ccagctgcc aactcgatgc tataagagat gcagaaattc ttcgtaaggc aatgaagggt 660
tttgggacag atgagcaggc aattgtggat gtggtggcca accgttccaa tgatcagagg 720
caaaaaatta aagcagcatt taagacctcc tatggcaagg atttaataca agatctcaaa 780
tcagagttaa gtggaaatat ggaagaactg atcctggccc tcttcattgcc tctacgtat 840
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cgtttacttg tgtccatgtg ccagggaat cgtgatgaga accagagtat aaaccaccaa 1080
atggctcagg aagatgctca gcgtctctat caagctgggt aggggagact agggaccgat 1140
gaatcttgct ttaacatgat ccttgccaca agaagcttct ctcagctgag agctaccatg 1200
gaggcttatt ctaggatggc taatcg agac ttgttaagca gtgtgagccg tgagttttcc 1260
ggatatgtag aaagtgggtt gaagaccatc ttgcagtgtg ccctgaaccg ccctgccttc 1320
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taaccgaaag agctttctgt caaggaccgt atcagggtaa tgtgcttggt ttgcacatgt 1680
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aataattttt tagaagggtt ctgaaaagctc tgccctcccg aatccctcta agtctgcttg 1920
atagagtggg tagtatgtta aaactgtgta ctttaaaaaa aaattcaacc tttacatcta 1980
gaataatttg catctcattt tgcctaaatt ggttctgtat tcataaacac tttccacata 2040
gaaaatagat tagtattacc tgtggcacct ttaagaaag ggtcaaagt tta tatgctt 2100
aagatacata gcctcccttt ttttcgctt gtttcccttt ttttaattga gttatgacaa 2160
ataaaaaatt gcatat 2176

```

<210> 216  
<211> 525  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(525)  
<223> 3' terminal sequence. thrombospondin 1  
(THBS1) gene.

<400> 216  
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attcaggagt gtgacaagag atttaaacag gatgggtggct ggagcntgng ttccccgtgg 120  
tcatcttgtt ctgtgacatg tggatggtt gtgatcacia ggatccggct ctgcaactct 180  
cccagcccc agatgaacgg gaaaccctgt gaaggcgaag gcgngagac caaagcctgc 240  
aagaaagacg cctgccccag taagtgtgag gtccgtgca aggtgagca tgggcagcag 300  
ctctgccag ctggttgctt gggcatct gc agcctgcagt ttcagtggg tcataggagc 360  
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tctttttaat tgaaaaacaa attcacntt ttccccagct ttttttcctt gtgttcaggg 480  
gaggcagagg ttttttgaac gggnttaggg gatttttgnc aagtt 525

<210> 217  
<211> 5722  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(5722)  
<223> thrombospondin 1 (THBS1) gene.

<400> 217  
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tctggcgcc gactggtgaa gggccc cgac ccttcagcc cagctttccg catcgaggat 300  
gccaacctga tccccctgt gctgatgac aagttccaag acctggtgga tgctgtgcgg 360  
gcagaaaagg gtttcctcct tctggcatcc ctgaggcaga tgaagaagac ccgggggcacg 420  
ctgctggccc tggagcggaa agaccactct ggccaggctc tcagcgtggt gtccaatggc 480  
aaggcgggca ccttgacact cagcctgacc gtccaaggaa agcagcacgt ggtgtctgtg 540  
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caaagcgtct tcaccagaga cctggccagc atcgccagac tccgca tcgc aaaggggggc 720  
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143/292

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&lt;210&gt; 218

&lt;211&gt; 397

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(397)

<223> 3' terminal sequence. protein tyrosine  
phosphatase, non-receptor type 2 (PTPN2) gene.

&lt;400&gt; 218

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ctcctaattt atttcttgta catctttcta catttcatac actcattaaa aacacttaac 120  
acatccaatt aaaggttctg caaagtcttc tgctggtggg tgctcttcat cccttggnt 180  
gtaaagttta ctttgtaaac aaacaactgt gaggncaatc tagaggggta ggcgagcctc 240  
actttagttt cgggagtggg gcttcagggt cttgctttgc acatcaatgg gttcaaaatt 300  
tataggctgc aggaatattc tcaaggatc ggaatattag ggngtctggt ncaat cttgg 360  
ggcccttttt tcttttttgg ttncatttct ccattta 397

&lt;210&gt; 219

&lt;211&gt; 338

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(338)

<223> 5' terminal sequence. protein tyrosine  
phosphatase, non-receptor type 2 (PTPN2) gene.

&lt;400&gt; 219

ggctccttga accctgacca tgggcctgcg gtgatccact gtagtgacag cattgggcgc 60  
tctggcacct tctctctggt agacacttgt cttgttttga tggaaaaagg agatgatatt 120  
aacataaaac aagtgttact gaac atgaga aaataccgaa tgggtcttat tcagacccca 180  
gatcaactga gattctcata catggctata atagaaggag caaatgtat aaagggat 240



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cattncacca aacaaaataa tgactgaaaa atacantg 338

<210> 220  
<211> 2287  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(2287)  
<223> protein tyrosine phosphatase, non -receptor  
type 2 (PTPN2) gene.

<400> 220  
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ctgtacttgg aaattcgaaa tgagtcccat gactatcctc atagagtggc caagtttcca 180  
gaaaacagaa atcgaaacag atacagagat gtaagcccat atgatcacag tctgtgttaa 240  
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tcaggtaaac agttggtcaa gactttgtaa agaaattggg ttctgtaaat cccattattg 2160  
atatgtttat ttttcatgaa aatttc aatg tagttggggg agattatgat ttaggaagca 2220  
aaagtaagaa gcagcatttt atgattcata atttcagttt actagactga agttttgaag 2280  
taaaccc 2287

<210> 221

<211> 296  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(296)  
<223> 3' terminal sequence. epha2 (EPHA2) gene.

<400> 221  
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actgtacgtg actgcaacag cttccctggg tggcgccant tcttggaag gagactttca 240  
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<210> 222  
<211> 3921  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(3921)  
<223> epha2 (EPHA2) gene.

<400> 222  
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gggtgtgcgg gagccgggct cggggggatc ggaccgagag cgagaagcgc ggcattggagc 120  
tccaggcagc ccgcgcctgc ttcgccctgc tgtggggctg tgcgctggcc gcggccgcgg 180  
cggcgagagg caaggaagtg gtactgtctg actttgctgc agctggaggg gagctcggct 240  
ggctcacaca cccgtatggc aaagggtggg acctgatgca gaacatc atg aatgacatgc 300  
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acaccattgc gcccgatgag atcacgctca gcagcgactt cgaggcacgc cacgtgaagc 600  
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agttgcagat gattcaaacc g 3921

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&lt;210&gt; 223

&lt;211&gt; 437

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(437)

<223> 3' terminal sequence. tissue inhibitor of  
 metalloproteinase 1 (erythroid potentiating  
 activity, collagenase inhibitor) (TIMP1) gene.

&lt;400&gt; 223

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ggaacagggt ggacactgtg caggcttcag cttccactcc gggcaggatt caggctatct 60
gggaccgcag gacttgccag gngcacagcc ctggctccc aggcaggcag gcaaggtgac 120
gggactggaa gcccttttca naggcttga ggagctggnc cgtccacaag caatgagtgc 180
cactctgcag tttgcagggg atggataaac agggaaacac tgtgcattcc tcacagcaa 240

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cagtntaggt cttggtnaag ccccggcgct gagctaagct caggcttttc caggggagcc 300  
acgaaactnc aggtagtgtat gtgcaagagt ccacccctgca gttttccagc aatnagaaac 360  
tcctcggttng cgggttttgg ggacnnttgg aagtnttc cg cagacatttt tccatgggccc 420  
gggttttaag acgaacc 437

&lt;210&gt; 224

&lt;211&gt; 466

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(466)

<223> 5' terminal sequence. tissue inhibitor of  
metalloproteinase 1 (erythroid potentiating  
activity, collagenase inhibitor) (TIMP1) gene.

&lt;400&gt; 224

gccncagatc cagcgcccag agagacacca gagaaccac catggccccc tttgnagccc 60  
ctggcttctg gcacccctgtt g ttgctgtgg ctgatagccc ccagcagggc ctgcacctgt 120  
gtcccacccc acccacagac ggcccttctgc aattccgacc tcgtcatcag ggccaagtgc 180  
gtggggacac cagaagtcaa ccagaccacc ttataccagc gttatgagat caagatgacc 240  
aagatgtata aagggttcca agccttaggg gatgccgctg acatccggtt cgtctacacc 300  
cccgccatgg agagtgtctg cggatacttn cacagggtccc acaaccgnag cgaggagttt 360  
ctcattngct ggaaaactgt aggatggact tcttgacat tnactacctt gcagtttng 420  
tgggttcctt gggaacagtc tgaggtttag ttnagcggtn ggggtt 466

&lt;210&gt; 225

&lt;211&gt; 782

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(782)

<223> tissue inhibitor of metalloproteinase 1  
(erythroid potentiating activity, collagenase  
inhibitor) (TIMP1) gene.

&lt;400&gt; 225

aggggcctta gcgtgccgca tcgccgagat ccagcgccca gagagacacc agagaaccca 60  
ccatggcccc ctttgagccc ctggcttctg gcacccctgtt gttgctgtgg ctgatagccc 120  
ccagcagggc ctgcacctgt gtcccacccc acccacagac ggcccttctgc aattccgacc 180  
tcgtcatcag ggccaagtgc gtggggacac cagaagtcaa c cagaccacc ttataccagc 240  
gttatgagat caagatgacc aagatgtata aagggttcca agccttaggg gatgccgctg 300  
acatccggtt cgtctacacc cccgccatgg agagtgtctg cggatacttc cacagggtccc 360  
acaaccgcag cgaggagttt ctcattgctg gaaaactgca ggatggactc ttgcacatca 420  
ctacctgcag tttcgtggct ccctggaaca gcctgagctt agctcagcgc cggggcttca 480  
ccaagacctt cactgttggc tgtgaggaat gcacagtgtt tccctgttta tccatcccct 540  
gcaaactgca gagtggcact cattgcttgt ggacggacca gctcctccaa ggctctgaaa 600  
agggttcca gtcccgtcac cttgcctgcc tgccctggga gccagggctg tgcacctggc 6 60  
agtccctgcg gtcccagata gcctgaatcc tgcccggagt ggaactgaag cctgcacagt 720  
gtccaccctg ttcccactcc catctttctt ccggacaatg aaataaagag ttaccacca 780

gc

782

<210> 226  
<211> 353  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(353)  
<223> 5' terminal sequence. ephrin -a1 (EFNA1)  
gene.

<400> 226  
acagctacta ctacatctca gccaaaccca tccaccagca tgaagaccgc tgcttgaggt 60  
tgaagggtgac tgtcagtggc aaaatcactc acagtcctca ggcccatgtc aatccacagg 120  
agaagagact tgcagcagat gaccagagg tgccgggttct acatagcatc ggtcacagtg 180  
ctgccccacg cctcttccca cttgcctgga ctgtgctgct ccttccactt ctgctgctgc 240  
aaaccccggtg aagggtgtatg ccacacctgg ccttaaagag ggaca ggctg aagagaggga 300  
caggcactcc aaacctgtct tgggggccac ttccagagcc ccagccctt ggg 353

<210> 227  
<211> 1480  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(1480)  
<223> ephrin-a1 (EFNA1) gene.

<400> 227  
gcggagaaag ccagtgggaa ccagaccca taggagacc gcgtccccgc tcggcctggc 60  
caggccccgc gctatggagt tcctctgggc ccctctcttg ggtctgtgct gcagtctggc 120  
cgctgctgat cgccacacgg tcttctggaa cagttcaaact cccaagttcc ggaatgagga 180  
ctacaccata catgtgcagc tgaatgacta cgtggacatc atctgtccgc actatgaaga 240  
tcactctgtg gcagacgctg ccatggagca gtacatactg tacctggtgg agcatgagga 300  
gtaccagctg tgccagcccc agtccaagga ccaagtccgc tggcagtga accggcccag 360  
tgccaagcat ggcccggaga agctgtctga gaagttccag cgcttcacac ctttcaccct 420  
gggcaaggag ttcaaagaag gacacagcta ctactacatc tccaaaccca tccaccagca 480  
tgaagaccgc tgcttgaggt tgaagggtgac tgtcagtggc aaaatcactc acagtcctca 540  
ggcccatgtc aatccacagg agaagagact tgcagcagat gaccagagg tgccgggttct 600  
acatagcatc ggtcacagtg ctgccccg cctcttccca cttgcctgga ctgtgctgct 660  
ccttccactt ctgctgctgc aaaccccggtg aagggtgtatg ccacacctgg ccttaaagag 720  
ggacaggctg aagagaggga caggcactcc aaacctgtct tggggccact ttccagagccc 780  
ccagccctgg gaaccactcc caccacaggc ataagctatc acctagcagc ctcaaaacgg 840  
gtcagtatta aggttttcaa ccggaaggag gccaaaccagc ccgacagtgc catccccacc 900  
ttcacctcgg agggacggag aaagaagtgg agacagtcct ttcccaccat tctgccttt 960  
aagccaaaga aacaagctgt gcaggcatgg tcccttaagg cacagtggga gctgagctgg 1020  
aagggggccac gtggatgggc aaagcttgct aaagatgccc cctccag gag agagccagga 1080  
tgccagatg aactgactga aggaaaagca agaaacagtt tcttgcttgg aagccaggta 1140  
caggagaggc agcatgcttg ggctgaccca gcattctcca gcaagacctc atctgtggag 1200  
ctgccacaga gaagtttgta gccaggtact gcattctctc ccattcctgg gcagcactcc 1260

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ccagagctgt gccagcaggg g ggctgtgcc aacctgttct tagagtgtag ctgtaagggc 1320
agtgcccatg tgtacattct gcctagagtg tagcctaaag ggcagggccc acgtgtatag 1380
tatctgtata taagttgctg tgtgtctgtc ctgatttcta caactggagt ttttttatac 1440
aatgttcttt gtctcaaaat aaagcaatgt gttttttcgg 1480

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&lt;210&gt; 228

&lt;211&gt; 170

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(170)

<223> 3' terminal sequence. endothelin receptor  
type a (EDNRA) gene.

&lt;400&gt; 228

```

ttttaagggt tctgtaaact tttattttac acttatgggc cactgcaact cagggccttg 60
gcttctggct catttctaca aagttaactt ttgaaaagat gtagtaaagg tagaaattgg 120
aaatatctct gctagtaaac cacagttact taccagtcca taaataaaat 170

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&lt;210&gt; 229

&lt;211&gt; 4105

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(4105)

&lt;223&gt; endothelin receptor type a (EDNRA) gene.

&lt;400&gt; 229

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gaattcgagg ccgcctcttg cggctccaga gtggagtgga aggtctggag ctttgggagg 60
agacggggag gacagactg g aggcgtgttc ctccggagtt ttctttttcg tgcgagccct 120
cgcgcgcgcg tacagtcac cgcctggctc gacgattgtg gagaggcggt ggagaggctt 180
catccatccc acccggtcgt cgcgggggat tgggggtccc ggcacacctc cccgggagaa 240
gcagtgccca ggaagttttc tgaagccggg gaagctgtgc agccgaagcc gccgcccgcg 300
cggagcccgg gacaccggcc accctccgcg ccacccaccc tcgctttctc cggcttctc 360
tgcccaggc gccgcgcgga cccggcagct gtctgcgcac gccgagctcc acggtgaaaa 420
aaaaagtga ggtgtaaaag cagcacaagt gcaataagag atatttcctc aaatttgct 480
caagatgaa accctttgcc tcagggcac cttttggct g gcaactgggtg gatgtgtaat 540
cagtgataat cctgagagat acagcacaat tctaagcaat catgtggatg atttcaccac 600
ttttcgtggc acagagctca gcttctgtg taccactcat caaccacta atttggtcct 660
accagcaat ggtcfaatgc acaactattg cccacagcag actaaaatta cttcagcttt 720
caaatacatt aacactg tga tatctgtac tattttcac gtgggaatgg tggggaatgc 780
aactctgtc aggatcattt accagaacaa atgtatgagg aatggcccca acgcgtgat 840
agccagtctt gcccttgagg accttatcta tgtggtcatt gatctcccta tcaatgtatt 900
taagctgctt gctgggcgct ggcttttga tcacaatgac tttggcgat ttctttgca a 960
gctgttcccc tttttgcaga agtcctcggt ggggatcacc gtctcaacc tctgcgctct 1020
tagtggtgac aggtacagag cagttgcctc ctggagtcgt gttcagggaa ttgggattcc 1080
tttgtaact gccattgaaa ttgtctccat ctggatcctg tcctttatcc tggccattcc 1140
tgaagcgatt ggcttcgtca tggtaacctt tgaa tatagg ggtgaacagc ataaaacctg 1200
tatgtcfaat gccacatcaa aattcatgga gttctaccaa gatgtaaagg actggtggct 1260

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cttcgggttc tatttctgta tgcccttggg gtgcaactgg atcttctaca cctcatgac 1320
ttgtgagatg ttgaacagaa ggaatggcag cttgagaatt gccctcagtg aacatcttaa 1380
gcagcgtcga gaagtggcaa aaacagtttt ctgcttgggt gtaatttttg ctctttgctg 1440
gttccctctt cacttaagcc gtatattgaa gaaaactgtg tataacgaaa tggacaagaa 1500
ccgatgtgaa ttacttagtt tcttactgct catggattac atcggtatta acttggcaac 1560
catgaattca tgtataaacc ccatagctct gtattttgtg agcaagaa at ttaaaaattg 1620
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catgaacgga acaagcatcc agtggagaa ccacgatcaa aacaaccaca acacagaccg 1740
gagcagccat aaggacagca tgaactgacc acccttagaa gcactcctcg gtactcccat 1800
aatcctctcg gagaaaaaaa tc acaaggca actgtgactc cgggaatctc ttctctgac 1860
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ctggtttatc caccacaac atctacgaat cgtacttctt taattgatct aatttacata 1980
ttctgctgtc tgtattcagc actaaaaaat ggtgggagct gggggagaat gaagactgtt 2 040
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aatagtattc aggtgagcaa ttagattagt attttccacg tcactattta tttttttaa 2400
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atgggtgttt attacaaggg acctgaaca tgtttgtat gttaaattca aaagtaatgc 2580
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ttcccttttc catataggaa acat aatttt gaagtggcca gatgagtta tcatgtcagt 2940
gaaaaataat taccacaaa tgccaccagt aacttaacga ttcttactt cttgggggtt 3000
tcagtagtaa cctaactccc caccocaaca tctccctccc acattgtcac catttcaaag 3060
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gtctgagcta aaatctaggt gattgttcat catgacaa cc tgcctcagtc cattttaacc 3360
tgtagcaacc ttctgcattc ataaatcttg taatcatgtt accattaca atgggatata 3420
agaggcagcg tgaaagcaga tgagctgtgg actagcaata taggggtttg tttgggttgt 3480
tggtttgata aagcagtatt tggggtcata ttgtttctcg tgctggagca aaagtcatta 3540
cactttgaag taattatatt ttcttatcct caattcaatg tggatgaa attgccaggt 3600
tgtctgatat ttctttcaga cttcgccaga cagattgctg ataataaatt aggtgaagata 3660
atttgttggg ccataatttt ggacaggtaa aataacatca ggttccagtt gcttgaattg 3720
caaggctaag aagtactgcc cttttgtgtg ttagcagtc aatctattat t cactggcg 3780
catcatatgc agtgatatat gcctataata taagccatag gtccacaca tttgttttag 3840
acaattgtct tttttcaag atgctttgtt tctttcatat gaaaaaaatg cattttataa 3900
attcagaaag tcatagattt ctgaaggcgt caacgtgcat tttatttatg gactggtaag 3960
taactgtggt ttactagcag gaatat ttcc aatttctacc ttactacat cttttcaaca 4020
agtaactttg tagaaatgag ccagaagcca aggcctgag ttggcagtg cccataagtg 4080
taaaataaaa gtttacagaa acctt 4105

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&lt;210&gt; 230

&lt;211&gt; 240

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(240)

<223> 3' terminal sequence. growth factor  
receptor-bound protein 2 (GRB2) gene.

<400> 230

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ggtttcttgt tttttattat tggcgctcagt agngactata cgtggcctta aacgtcatgc 60
actgatggac agaagagaaa aaaggatgaa aaaaaagaca aaggagggga aagaggagca 120
gcagtgaan tttgtaataa aaactcttct taatttatag gtaagttttg gcatttttaa 180
atccaacgcc cctoccacc ccctaaagt ccaaccaag tgagaggggc acagggtgac 240
```

<210> 231

<211> 475

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(475)

<223> 5' terminal sequence. growth factor  
receptor-bound protein 2 (GRB2) gene.

<400> 231

```
cttaatggaa aagacggctt cattcccaag aactacatag aaatga aacc acatccgtgg 60
ttttttggca aaatccccag agccaaggca gaagaaatgc ttagcaaaca gcggcacgat 120
ggggccttct ttatccgaga gagtgaagc gctcctggg acttctccct ctctgtcaag 180
tttgaaaacg atgtgcagca ctcaagggtg ctccgagatg gagccgggaa gtacttcctc 240
tggttggtga agttcaattc ttga atgag ctggtggatt atcacagatc tacatctgtc 300
tccagaaacc agcagatatt cctgcgggga cattaggaac aggtgccaca gcaggccgac 360
atacgttcca ggggcctttt ttgattttt gattccccag gggggnttgg ngaggttggg 420
ttttccgccg ggggagattt tattccatgt tcntgggtn aatttaggaa ccntt 475
```

<210> 232

<211> 1109

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(1109)

<223> growth factor receptor -bound protein 2  
(GRB2) gene.

<400> 232

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gccagtgaat tcgggggct c agccctctc cctcccttcc ccctgcttca ggctgctgag 60
cactgagcag cgctcagaat ggaagccatc gccaaatatg acttcaaagc tactgcagac 120
gacgagctga gcttcaaaag gggggacatc ctcaagggtt tgaacgaaga atgtgatcag 180
aactggtaca aggcagagct taatggaaaa gacggcttca ttccaagaa ctacatagaa 2 40
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agcaaacagc ggcacgatgg ggcctttctt atccgagaga gtgagagcgc tcctggggac 360
ttctccctct ctgtcaagtt tggaaacgat gtgcagcact tcaagggtgct ccgagatgga 420
gccgggaagt acttccctctg ggtgtgaag ttcaattctt tgaatgagct ggtggattat 480
cacagatcta catctgtctc cagaaaccag cagatattcc tgcgggacat agaacagggtg 540
ccacagcagc cgacatacgt ccaggccctc tttgactttg atccccagga ggatggagag 600
ctgggcttcc gccggggaga ttttatccat gtcattgata actcagacc caactggtgg 660
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```

aaaggagctt gccacggg ca gaccggcatg tttccccgca attatgtcac ccccgtagac 720
cggaacgtct aagagtcaag aagcaattat ttaaagaaag tgaaaaatgt aaaacacata 780
caaaagaatt aaaccacaa gctgcctctg acagcagcct gtgagggagt gcagaacacc 840
tggccgggtc accctgtgac cctctcactt tgggttggaac tttagggggg gggagggggc 900
gttggaattt aaaatgccaa aacttaccta taaattaaga agagttttta ttacaaattt 960
tcaactgctg tcctctttcc cctcctttgt cttttttttc atcctttttt ctcttctgtc 1020
catcagtgca tgacgtttta ggccacgtat agtcctagct gacgccaata ataaaaaaca 1080
agaaaccaaa aaaaaaaaaa ccgaattca 1109

```

&lt;210&gt; 233

&lt;211&gt; 446

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(446)

<223> 3' terminal sequence. jun d proto -oncogene  
(JUND) gene.

&lt;400&gt; 233

```

cgcgcgctct ggctgccnng ntgtacaccg cgccggaaag tggggctcog agggggcgca 60
ctcaaaaccc tgcctttcct ttacttttac tttttttttt ttttctttgg aagagagaag 120
aacagagtgt tcgattctgc cctatttatg tttctactcg ggaacaaacg ttggttgtgt 180
gtgtgtgtgt tttcttgtgt tgggttttta a agaaatggg aagaagaaaa aaaaattctc 240
cgcccccttc ctgatctcg ctccccctt cggttcttcc gaccgggtcc cccctccctt 300
ttttgtttct gttttgtttt gttttgctac gagtccacat tcctgtttgt aatccttggg 360
ttcgnccggg tttctgtttt cagtaaagtc tcgttacggc aaaacctcgt gccgaatttt 420
tggggctcga ggggcaaaat ttcca 446

```

&lt;210&gt; 234

&lt;211&gt; 1891

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1891)

&lt;223&gt; jun d proto -oncogene (JUND) gene.

&lt;400&gt; 234

```

ccgaggctat aagaggggcg acaagtggcg cgcgcgagga gccgcccga gtggagggcc 60
ggcgctgctg gccgcccgcg gggcgggcg agggccgagc ggacgggggg gcgcccggcc 120
cccgggaggg cgcgccact cccccccggg ccggcgcgcg gggggaggcg gaggatggaa 180
acacccttct acggcgatga ggcgctg agc ggccctggcg gcggcgccag tggcagcggc 240
ggcacgttcg cgtccccggg ccgcttggtc cccggggcg ccccgacggc cgcggccggc 300
agcatgatga agaaggacgc gctgacgctg agcctgagtg agcaggtggc ggcagcgctc 360
aagcctgcgc ccgcgcccgc ctccctaccc cctgcgcgcg acggcgcccc cagcgcgcca 420
ccccccgacg gctgctcgc ctctcccgac ctggggctgc tgaagctggc ctccccgag 480
ctcagcgccc tcatcatcca gtccaacggg ctggtcacca ccacgccgac gagctcacag 540
ttcctctacc ccaaggtggc ggccagcgag gacgaggagt tcgcccaggg ctctgtcaag 600
gccctggagg atttacacaa gcagaaccag ctggcgcgcg gccgggc cgc tgcgcccgc 660
gccgcccgcg ccggggggcg ctcgggcacg gccacgggct ccgcgcccc cgcgagctg 720

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```
gccccggcgg cgccgcgcgc cgaagcgcc gtctacgcga acctgagcag ctacgcgggc 780
ggcgccgggg gcgcgggggg cgccgcgacg gtgcgcttcg ctgcggaacc tgtgcccttc 840
ccgcgcgcgc caccgccagg cgcg tgggg ccgcgcgcgc tggctgcgct caaggacgag 900
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cagctcaagc agaaagtcc cagccacgtc aacagcggct gccagctgct gcccagcac 1200
caggctccgg cgtactgagt cgggcatggc ggccacctcc aaggggcggg ctgcggggg 1260
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aaccctgcct ttcctttact tttactttt tttttcttt ggaagagaga agaacagagt 1620
gttcgattct gccctattta tgttctact cggggaacaa acgttggtg tgtgtgtgtg 1680
tgtttcttg tgttggttt ttaaagaaat aaaaaaaat ctcc gccct 1740
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tgttttgtt tgttttgta cgagtccaca ttctgtttg taatccttg ttcgcccgt 1860
tttctgttt cagtaaaagtc tcgttacgcc a 1891
```

&lt;210&gt; 235

&lt;211&gt; 421

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(421)

<223> 3' terminal sequence. swi/snf related,  
matrix associated, actin dependent regulator of  
chromatin, subfamily a, member 2 (SMARCA2) gene.

&lt;400&gt; 235

```
acaaaaagtc ttcaagccac gagcggaggg cattcctgca ggccatcttg gagcatgagg 60
aggaatatga ggaagaagat gaagtaccgg acgatgagac tctgaaccaa atgattgctc 120
gacgagaaga agaatttgac ctttttatgc ggatggacat ggaccggcgg agggaagatg 180
ccggaaccc gaaacggaag cccggttaa tgaggagga tgagctgcc tctggntca 240
ttaaggatga cgctgaagta gaaaggctca cctgtgaaga agaggaggag aaaatatgtg 300
ggagggggtc ccgccagcgc cgtgacgtgg actacagtga cgccctcacg gagaagcagt 360
ggctaaaggg cntcgaaga cggcattng gaggaattng aagaggaata c ggttaagaa 420
g 421
```

&lt;210&gt; 236

&lt;211&gt; 438

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(438)

<223> 5' terminal sequence. swi/snf related,  
matrix associated, actin dependent regulator of

chromatin, subfamily a, member 2 (SMARCA2) gene.

<400> 236

```
tggaatttt ctgccgggca ctcttaaaca ctgactgtaa gacgatggag tcttcataga 60
tctgggatcc ctccaggttg aacgtctgag cg ttgtgaca gagaagcatg acatccttct 120
ccaggtcgcc taggctccgg tacttatgat tacgaatcct ttccctttatt tttttgaaat 180
ccactggctt cctaattaat tcatagtatt ctggtaattc ttcccttgaa ggtaactgaa 240
tgaagacttc actgagctgt cgccctgaac tgtttccttc tttttccaac tgagaattac 300
tgggcacctt ctccacgtta cacctatctt tgtagtttat cacagtattc gatgattagc 360
gttcatctgg ctttgtcagt ttggggggga tttggtgaca gntttntcag cgggagggcg 420
gcctcttctc ttcttagg                                438
```

<210> 237

<211> 5257

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(5257)

<223> swi/snf related, matrix associated, actin  
dependent regulator of chromatin, subfamily a,  
member 2 (SMARCA2) gene.

<400> 237

```
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ctgatgaaga tgtgtctgatt aacatattct gtgatatggt ttacaacttt taatcataat 120
tgtccatgat tttggaatgc tgttatattat cagtaaatgt aaaatatttg aggcatttag 180
ccatacacac actagaactt tttaaaactt tgtoctatag tgtaatta ta aactgatgac 240
tattatcttc atacattgag tcttcatgca tcaatgaaat gaaaaatata ggagtagatg 300
tccacgcccc cagaccctgg tgcgatgccc caccaggggc cttcgccggg gcctgggcct 360
tcccctgggc caattcttgg gcctagtcca ggaccaggac catccccagg ttccgtccac 420
agcatgatgg ggccaagtcc tggacc tcca agtgtctccc atcctatgcc gacgatgggg 480
tccacagact tcccacagga aggcattgat caaatgcata agcccatcga tggatatacat 540
gacaagggga ttgtagaaga catccattgt ggatccatga agggcactgg tatgcgacca 600
cctcaccagg gcatggggcc tcccagagt ccaatggatc aacacagcca aggttatatg 660
tcaccacacc catctccatt aggagcccc gagcacgtct ccagccctat gtctggagga 720
ggccccactc cacctcagat gccaccaagc cagccggggg cctcatccc aggtgatccg 780
caggccatga gccagcccaa cagaggtccc tcacctttca gtectgtcca gctgcatcag 840
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caacagcagc agcagcagca gcagcagcag cagcagcagc agcaacagca gccgcagcag 1020
cagccgcccg aaccacagac gcagcaacaa cagcagccgg ccttggttaa ctacaacaga 1080
ccatctggcc cggggccgga gc tgagcggc cccagcaccg cgcagaagct gccggtgccc 1140
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gtgcccgggc cctcagtgcc gcagccggcc cccggggcag cctcgcccggt cctccagctg 1260
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agaatgcggc gactgatggc tgaagatgag gagagttata gaaaactgat tgatcaaaag 1860
aaagacaggc gtttagctta ctttttgacg cagaccgatg agtatgtagc caatctgacc 1920
```

aatctggttt gggagcacia gcaagcccag gcagccaaag agaagaagaa gaggaggagg 1980  
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gagcccatag atgagagcag ccagatgagt gacctccctg tcaaagtac tcacacagaa 2100  
accggcaagg ttctgttcgg accagaagca cccaaagcaa gtcagctgga cgctggctg 2160  
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gtggaatatg tgatcaagt tgacatgtca gctctgcaga agattctgta tcgcatatg 3240  
caagccaagg ggtatcttct cacaga tgg tctgagaaag ataagaagg gaaaggaggt 3300  
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cgaggaaaag ccaaacctgt agtgagcgat tttgacagcg atgaggagca ggatgaacgt 4980  
gaacagtcag aaggaa gtgg gacggatgat gagtgatcag tatggacctt tttccttggg 5040  
agaactgaat tcttccctcc cctgtctcat ttctaccag tgagtccatt tgtcatatag 5100  
gcactgggtt gtttctatat catcatcgtc tataaactag ctttaggata gtccagaca 5160  
aacatatgat atcatggtgt aaaaaacaca cacatacaca aatatttgtg accaa atggg 5220  
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&lt;210&gt; 238

&lt;211&gt; 507

&lt;212&gt; DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(507)

<223> 3' terminal sequence. protein phosphatase 2  
(formerly 2a), regulatory subunit b (pr 52), gamma  
isoform (PPP2R2C) gene.

<400> 238

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tacatgctca cccgggacta ccttacagtc tatggatggg acctgaacat ggaggcaaga 60
cccatagaga cctaccaggt ccatgactac cttcggagca agctctgttc cctgtacgag 120
aacgactgca ttttcgacaa gtttgaatgt gcctggaacg ggagcgacan tncatcatga 180
ccggggccta caacaacttc ttccgcatgt tcgatcggaa caccaagcgg gacgtgaccc 240
tgaggagcct cgagggaag cagcaagccc cgggctgtgc tcaagccacg gcgcgtgtgc 300
gtgggggggc aagcgccggc gtgnatga ca tcagtgtggg acagcttggg acttcaccaa 360
gaagatcctg cacacggcct ggcacccggc tgaggaacat catttgccat tcgccccac 420
caacaacctg ttacatcttt ccaggggcaa ggtaaatttt tgacattgca ttaggtattn 480
tgcaatttcc cgnccttgc caacca 507
```

<210> 239

<211> 521

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(521)

<223> 5' terminal sequence. protein phosphatase 2  
(formerly 2a), regulatory subunit b (pr 52), gamma a  
isoform (PPP2R2C) gene.

<400> 239

```
taaacagaga attactgcca aacacaattc tggcctagga aagcggggnn gggagggggc 60
ccaaacttcc tgtgtccaca cactgccacc tctgcagctg tctcatcag tgggtgtgact 120
ttcttccctt ccttgcatgt cggtcgtgaa ggtcatgtcg gggatgactt gcatgaggct 180
gggtggcagg ggccgggaac tgcacatacc tagtgcattg cagagtttac cttgtcctgg 240
aagatgtaca ggttggtggt ggcggcgatg gcaatgatgt tctcagccgg gtgccaggcc 300
gtgtgcagga tcttcttggt gaagtccaag ctgttccaaa atgatgtcat cagccgggcc 360
cttgccccc acgnaaangg nccnttggtt tnagcaaagc ccng ggtttg ttgcttttcc 420
ctnagnagcn tncaggntca agtnccnttt ggtnttnccc gatcgaacat ncggaagaat 480
tttttttagg ccccntcat gatgaacgtg tncgttcct t 521
```

<210> 240

<211> 350

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(350)

<223> 3' terminal sequence. thrombospondin 3  
(THBS3) gene.

<400> 240

```
cagattcatt nnnnganntg cctgtgacaa ttgccccaac gttcccaaca atgaccagaa 60
ggacacagat ggcaatgggg aaggagatgc ctgtgacaac gac gtggatg gggatgggtg 120
aggcctgggg ctgaaggggt ggctggggga cctgtgagaa tttggatcag gtggggatga 180
agcaggggaag ctaggaagtc tctgtgaaat agggaggcag gcttntggac gttggcctgg 240
gtgaggagag attacctgca gcagatgtca ataggaatnt gaggtagggc gtagtnttag 300
gcagagtttg gactagaggg t nagacaaga aacaggcaga tttcctggcc 350
```

<210> 241

<211> 2871

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(2871)

<223> thrombospondin 3 (THBS3) gene.

<400> 241

```
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gccagtcagg atctgcaggT aattgacctg ctgactgtgg gcgagtctcg gcagatggta 120
gctgtggcag agaagatccg gacagccttg ctactgctg gggacatcta cctcttatcc 180
accttccgcc tgcccccaa gcagggtggT gtctctttt g cctctattc togccaagac 240
aacactcgat ggctggaggc ctctgttgta ggcaagatca acaaagtact ggtgcgatac 300
cagcgggagg atggcaaatg ccacgccgtg aacctacagc aagcgggcct ggctgatggg 360
cgcacacaca cagttctcct gcgactcoga ggtccctcca gacctagccc tgccctacat 420
ctctacgtgg actgcaaact gggtgacca catgcaggcc ttccagcact ggccccatt 480
cctccagcgg aggtcgatgg gctggagatt aggactggac agaaggcgta tttgaggatg 540
cagggctttg tggaatctat gaaaattatt ctgggtgggt ccatggccc ggtaggagcc 600
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cactccattc taggggagca gaccaaggcg ctggtcacc aactcaccct cttcaaccag 720
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aatccctgct tccgaggtgt ggactgcatg gaagtgtacg agtaccagc ctaccgctgt 900
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gcccggggca gcaaac aggt ctgcaatgac atcgatgaat gcaacgatgg caacaatggt 1140
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ccagcccaca gcccctgcca catccatgct cactgtctct ttgaacgcaa tgggtg cagtg 1320
tcttgcagat gtaacgtggg ctgggctggg aatgggaacg tgtgtgggac tgacacagac 1380
atcgatggct acccagacca agcactgccc tgcatggaca acaacaaaca ctgcaaacag 1440
gacaactgcc ttttgacacc caactctggg caggaagatg ctgataatga tgggtgtggg 1500
gaccagtgtg atgatgatgc tgatgggatg gggatcaaga atgttgagga caactgccgg 1560
ctgttcccca acaaagacca gcagaactca gatacagatt catttgggtg tgcctgtgac 1620
aattgcccc aagttcccaa caatgaccag aaggacacag atggcaatgg ggaaggagat 1680
gcctgtgaca acgacgtgga tggggatggc atccccaatg gattggacaa ttgccctaaa 1740
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cagctgcca atagctccca gctggactct gataacgatg gac ttggaga tgagtgtgat 1980
ggggatgatg acaatgatgg catcccagat tatgtgcctc ctggtccga taactgccgc 2040
```

158/292

```

ctggtaccca atcccaatca gaaggactca gatggcaatg gcgttggtga tgtgtgtgag 2100
gatgactttg acaatgatgc tgtggtcgac cccctggatg tgtgtcctga aagtgcagag 2160
gtaacgctta cggatttt cg ggcctatcag accgtcgctc tggatcctga gggatgatgct 2220
cagattgacc caaactgggt tgtgtcctcaac cagggcatgg aaatcggtca gaccatgaac 2280
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tgcttctccc aagaaaacat aatttgggtcc aatctccagt atcgatcaa tgacacagt 2820
cctgaggact ttgagccatt ccggaggcag ctgctccagg gaagggtgtg a 2871

```

&lt;210&gt; 242

&lt;211&gt; 509

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(509)

<223> 3' terminal sequence. actin, gamma 1 (ACTG1)  
gene.

&lt;400&gt; 242

```

cacttttatt tnccttaca caatgacgtg ttgctggggc ctaatgtntc cacataacag 60
tagaaaacca aaatttggtg tcatctcttc aaagantcga ganttgcgta caaaaaaac 120
cttacataan ttaagantga ntacatttac aggcgtaaat gcaaaccgnt tccaactcaa 180
agcaagtaac agcccaagggt gttctggcca aagacatcag ctaagaaagg aaactggggn 240
cctacggctt gggactttcc aacctgggac aggaccgca agncaaaac aactgggttc 300
ttgccagcct ctaggaggaa ttcccgaac actcaggccc tggacangtt taataccagg 360
ggggancagt taactttcan tacaggggnc aaaatcaggc aacagttt tt accantccag 420
tggctggttt cnggttacag gtttcagggt cattttnttt tcggagggtt tntcccggt 480
tcgtgagggt aggctgagggt tttntgctt 509

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&lt;210&gt; 243

&lt;211&gt; 393

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial S equence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(393)

<223> 5' terminal sequence. actin, gamma 1 (ACTG1)  
gene.

&lt;400&gt; 243

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gatcaccgcc ctggccccag caccatgaag atcaagatca tcgcaccccc agagcgcaag 60
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attagcaagc aggagtacga cgagtcgggc cctccatcg tccaccgcaa atgcttctaa 180
acggactcag cagatgcgta gattttgctg catgggttaa ttgagaatag aaatttgccc 240

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159/292

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atttttgacc ttgtantga agttaactg ttt 393

&lt;210&gt; 244

&lt;211&gt; 1919

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1919)

&lt;223&gt; actin, gamma 1 (ACTG1) gene.

&lt;400&gt; 244

gtctcagtcg ccgctgccag ctctcgcaact ctgttcttcc gccgctccgc cgtcgcgttt 60  
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aacattagga cccagcaaca cgtcattgtg taaggaaaaa taaaagtgt g ccgtaacc 1919

&lt;210&gt; 245

&lt;211&gt; 467

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer



<220>  
<221> misc\_feature  
<222> (1)..(467)  
<223> 3' terminal sequence. integrin, alpha 6  
(ITGA6) gene.

<400> 245  
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cctcttcggc ttctcgctgg ccatgcactg gcaactgcag cccgaggaca agcggctgtt 180  
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atgcttgacc ccacgtcaga aagcaaggaa gattagtgg atngggggtc aacgtccaga 360  
gccaaaggtt agggggcaag gtcgtgacat gtgttnacc tattgaaaa aggagcgtt 420  
ttattacgna gcangatttc cgagaca ttt ttgggcgttt tttttcc 467

<210> 246  
<211> 473  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(473)  
<223> 5' terminal sequence. integrin, alpha 6  
(ITGA6) gene.

<400> 246  
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cacatgtcac gaccttgccc cctggacctt ggctctggac ggtgaccccc atccactgat 180  
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gccagtgcac ggccacgca gaaagccgaa gaggttcccc ggggtnttcc atattttccg 420  
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<210> 247  
<211> 5611  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(5611)  
<223> integrin, alpha 6 (IT GA6) gene.

<400> 247  
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ccgtccctt ccccggtgct ccgccatgg ccgcgcgg gcagctgtgc ttgctctacc 180  
tgtcggcggt gctcctgtcc cg gctcggcg cagccttcaa cttggacact cgggaggaca 240  
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&lt;210&gt; 248

&lt;211&gt; 406

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(406)

<223> 3' terminal sequence. rad9 (s. pombe)  
homolog (RAD9) gene.

&lt;400&gt; 248

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&lt;210&gt; 249

&lt;211&gt; 2102

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2102)

&lt;223&gt; rad9 (s. pombe) homolog (RAD9) gene.

&lt;400&gt; 249

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at 2102
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&lt;210&gt; 250

&lt;211&gt; 365

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(365)

<223> 3' terminal sequence. activating  
transcription factor 3 (ATF3) gene.

&lt;400&gt; 250

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164/292

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 ctctt 365

&lt;210&gt; 251

&lt;211&gt; 453

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(453)

&lt;223&gt; 5' terminal sequence. activating transcription factor 3 (ATF3) gene.

&lt;400&gt; 251

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 tgcagtatct caagatattc aggtgggcca gaagagcttg tcagcaagag ggaggacag 300  
 aattctccca ggcgttaaca caaaatccat ggggcagtat ggatgggcag gtocttctgt 360  
 tggcaaacct agttcccaag tcacagggaa gganaggcag gaaagtttca actttcccaa 420  
 agggtttagg ggcttttcca cttcaatgtc tta 453

&lt;210&gt; 252

&lt;211&gt; 2056

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2056)

&lt;223&gt; activating transcription factor 3 (ATF3) gene.

&lt;400&gt; 252

gcagccaggc ggcactgca cagctctctt ctctcgccgc cgcccgagcg cacccttcag 60  
 cccgcgcgcc ggcctgagt cctcggtgct cgcccgccgc ccagacaaac agcccgcccg 120  
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 ctgtcagcga cagaccctc ggggtgtcca tcacaaaagc cgaggtagcc cctgaagaag 420  
 atgaaaaggaa aaagaggcga cgagaaagaa ataagattgc agctgcaaag tgccgaaaca 480  
 agaagaagga gaagacggag tgctgcagc ttcag tatta gcagagccac aggcgcctc 540  
 tgtggcatca ccagggtttc tctgaagaag agggctgtca ttttcctaaa ccagtgtctg 600  
 ctctcccatc tcccatcttc ctctgcagc ttgatgagcc ccggtgtgtc ccaggagtgc 660  
 gagaagctgg aaagtgtgaa tgctgaactg aaggctcaga ttgaggagct caagaacgag 720  
 aagcagcatt tgatatacat gctcaacctt catcggccca cgtgtattgt ccgggtcag 780

165/292

```

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aattctgatg tttctgtgaa attctcagag tgtttaattg tactcaatgg tatcattaca 1980
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aaatattgtg gtaaaa
2056

```

&lt;210&gt; 253

&lt;211&gt; 502

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(502)

<223> 3' terminal sequence. v-akt murine thymoma  
viral oncogene homolog 2 (AKT2) gene.

&lt;400&gt; 253

```

acatcatctc gtacatgacc acaccagcc cantacnntt tccacggccc ggccatagtc 60
attgtcctcc agcacctcag gcgccaggta ctccggggtc ccacagaagg ttttcatggt 120
ggccccgtca ctgatgccct ctttgacagag gccaaagtca gtgatcttga tgtggccatc 180
tttgtccagc atgagggtttt ccagcttgat gtgcggtat accacgtccc gcgagtgcaa 240
gtactcaaga gccagacaa tctctgcacc ataaaaccgg gcccgctcct ctgtgaagac 300
acgctcccg ggacagggtg gaagaacagc tcaccccggt tgggcatact ccattcaca 360
aggcacaggg cgggtcgtgg ggtctgggaa gggcattant ttcaggcggc agttgaggga 420
acgggggtgc nggggtgtt ctgggaggga cccggttttt cggttgattn ttttgaggcg 480
atthtcatcc nttgggcaat tt
502

```

&lt;210&gt; 254

&lt;211&gt; 1715

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1715)

<223> v-akt murine thymoma viral oncogene homolog  
2 (AKT2) gene.

<400> 254

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gaattccagc ggcgcgcgcg ttgccgctgc cgggaaacac aaggaaaggg aaccagcgc a 60
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ctgtgccctg tccacggtgc ctctgcatg tcctgctgcc ctgagctgtc ccgagctagg 180
tgacagcgta ccacgctgcc accatgaatg aggtgtctgt catcaaagaa ggctggctcc 240
acaagcgtgg tgaatacatc aagacctgga gccacagg ta ctctctgctg aagagcgacg 300
gtccttcat tgggtacaag gagaggcccg agggccctga tcagactcta ccccccttaa 360
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ttgtcatacg ctgcctgcag tggaccacag tcatcgagag gaccttccac gtggattctc 480
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ctgaggagat ggaagtggcg gtcagcaagg cacgggctaa agtgaccatg aatgacttcg 660
actatctcaa actccttggc aagggaacct ttggcaaagt catcctggtg cgggagaa gg 720
ccactggcgc ctactacgcc atgaagatcc tgcgaaagga agtcatcatt gccaaaggatg 780
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ttggtggggg gccagcgat gccaaaggagg tcatggagca caggttcttc ctacagcatca 1440
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aggtcgacac aaggtacttc gatgatgaat ttaccgcccc gtccatcaca atcacacccc 1560
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tctcctactc ggccagcatc cgcgagttag cagtctgccc acgcagagga cgcacgctcg 1680
ctgccatcac cgctgggtgg ttttttacc ctgcc 1715
```

<210> 255

<211> 431

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(431)

<223> 5' terminal sequence. s100 calcium-binding  
protein, beta (neural) (S100B) gene.

<400> 255

```
gagaggatgt ctgagctgga gaaggccatg gtggcctcat cgacgttttc caccaatatt 60
ctggaaggga gggagacaag cacaagctga agaaatccga actcaaggag ctcatcaaca 120
atgagcttcc ccatctctta gaggaaatca aagagcagga ggttgtggac aaagtcatgg 180
aaacactgga caatgatgga gacggcgaat gtgacttcca gggaattcat ggcctttgtt 240
gccatggtta ctactgcctg ccacgagttc ttgaacat g agtnagatta ggaaagcagc 300
caaacctttt cctgttaaca gaggacggtt catggcaaga naggcaggac aggcaagggg 360
tttgaggct tagttaggga gcttgagggt tttccagccg tntttnttg gttaatttag 420
ggaagggttg a 431
```

<210> 256

167/292

<211> 1095  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(1095)  
<223> s100 calcium-binding protein, beta (neural)  
(S100B) gene.

<400> 256  
tgccgcccag gaccgcgagc agagacg acg cctgcagcaa ggagaccagg aaggggtgag 60  
acaaggaaga ggaagtctga gctggagaag gccatggtgg ccctcatcga cgttttccac 120  
caatattctg gaagggaggg agacaagcac aagctgaaga aatccgaact caaggagctc 180  
atcaacaatg agctttccca tttcttagag gaaatcaaag agcaggagggt tgtggacaaa 240  
gtcatggaaa cactggacaa tgatggagac ggcgaatgtg acttccagga attcatggcc 300  
tttgttgcca tggttactac tgccctgccac gagttctttg aacatgagtg agattagaaa 360  
gcagccaaac ctttcctgta acagagacgg tcatgcaaga aagcagacag caagggcctt 420  
cagcctagta ggagctgagc tttccagccg tgtttagctt aattagga ag ctigatttgc 480  
tttgtgattg aaaaattgaa aacctcttc caaaggctgt ttaacggcc tgcattcttc 540  
tttctgctat attaggcctg tgtgtaagct gactggcccc agggactctt gttaacagta 600  
acttaggagt caggtctcag tgataaagcg tgcaccgtgc agcccgccat ggccgtgtag 660  
accctaaccg ggagggaacc ctgact acag aaattacccc ggggcaccct taaaacttcc 720  
actacottta aaaaacaaag ccttatccag cattatttga aaacactgct gttctttaa 780  
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tggtcttcggc ctgcttcccg ggatgcgcct gatcaccagg tgaacgctca gcgctggcag 900  
cgtcctggaa aaagcaactc catcagaact cgcaatccga gccagctctg ggggctccag 960  
cgtggcctcc gtgacctatg cgattcaagt cgcggctgca ggatccttgc ctccaacgtg 1020  
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gcgttcaata aaaag 1095

<210> 257  
<211> 542  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(542)  
<223> 3' terminal sequence. atp-binding cassette,  
sub-family b (mdr/tap), member 1 (ABCB1) gene.

<400> 257  
ttttaaaatc tactttaatt ctgttataaa atttataatg cagttttaaac tatgatttct 60  
ctocacttga tgatgtctct cactctgttc ctttaattac gaagtctctg aagactctga 120  
acttgactga ggaaatgtta aacagatacc tcttcataat tctgtaagt tttgctttta 180  
actttgaataaatgtcatat ctaaacaat attaaaaagt atttaacatc tcatacagtc 240  
agagttcact ggcgctttgt tccagcctgg aactgacca ttgaaaaata gatgcctttc 300  
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attaagtctg cattctggat ggtggacagg cggtagcaaa tcacaatgca ggtgcggcct 420  
tctctggcta tgccagggtc tcttgacaaa ctttttcacc tactgtatcc agagctgacg 480  
tggtcatcc aaaagcaaaa tantgggctg tctaacaagg gcacgagcta ttgccatgcg 540  
tt 542



<210> 258  
<211> 4643  
<212> DNA/RNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(4643)  
<223> atp-binding cassette, sub-family b  
(mdr/tap), member 1 (ABCB1) gene.

<400> 258  
cctactctat tcagatattc tccagatt cc taaagattag agatcatttc tcattctcct 60  
aggagtactc acttcaggaa gcaaccagat aaaagagagg tgcaacggaa gccagaacat 120  
tcctctctgga aattcaacct gtttcgcagt ttctcgagga atcagcattc agtcaatccg 180  
ggccgggagc agtcatctgt ggtgaggctg attggctggg caggaacagc gccggggcgt 240  
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gaacaataaa agtgaaaaag ataagaagga aaagaaacca actgtcagtg tattttcaat 540  
gtttcgctat tcaaattggc ttgacaagtt gtatatggtg gtgggaactt tggctgccat 600  
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gataggctgg tttgatgtgc acgatgttg ggagcttaac acccgactta cagatgatgt 960  
ctccaagatt aatgaaggaa ttggtgacaa aattggaatg ttctttcagt caatggcaac 1020  
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aaatggaggc ctgcaaccag catttgcaat aatattttca aagattatag gggtttttac 2640  
aagaattgat gatcctgaaa caaacgcaga gaatagtaac ttgttttcac tattgtttct 2700

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gccttgctaa agatttatag aagta gcaaa aagtattgaa atgtttgcat aaagtgtcta 4620
taataaaact aaactttcat gtg 4643

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&lt;210&gt; 259

&lt;211&gt; 486

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(486)

<223> 3' terminal sequence. selectin e  
(endothelial adhesion molecule 1) (SELE) gene.

&lt;400&gt; 259

```

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aaaattataa aatattttta gttataatct aaaattctca ataaaactca aacacaaacc 1 20
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aacaatttca agaaaaataa cactgtattc catacatagc ctgatcacag tagttgttct 240
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atcacatctc tgttttgact gttgggcttt ggttgggtgc cagtgggttc gccagggaact 360
tctctgggaa actttttttt tcaacactgg ctagggtang gggngttag gggggnggt 420
ttggtttcnt cacantccct cagggtnggg ggcgggttng ggnattacc ggcgggggt 480
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<210> 260  
<211> 478  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(478)  
<223> 5' terminal sequence. selectin e  
(endothelial adhesion molecule 1) (SELE) gene.

<400> 260  
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agaggaaaaa aatgactaaa aatattatta acttaaaaaa tggacagggtg ttggatgccc 420  
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<210> 261  
<211> 3834  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(3834)  
<223> selectin e (endothelial adhesion molecule 1)  
(SELE) gene.

<400> 261  
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ttgcttcaca gttctctca gctctcactt tgggtgcttct cattaagag agtggagcct 180  
ggtcttaca cacctccacg gaa gctatga cttatgatga ggccagtgtt tattgtcagc 240  
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&lt;210&gt; 262

&lt;211&gt; 267

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(267)

&lt;223&gt; 3' terminal sequence. epidermal growth factor (beta-urogastrone) (EGF) gene.

&lt;400&gt; 262

gtttatgttt ttggtgattt tatttaaata attagaagaa attcatcggt gt ctataatg 60

172/292

```

aaaacaaatc aggcaattta cttacaatct tgtaactgaa aatacatata aattctgtgc 120
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aagcctcctg tgtaatatct taaaatanaa tgttttcatt caaatatctt aaaaaataag 240
natctaactc gaaaaaatca gtttcta 267

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&lt;210&gt; 263

&lt;211&gt; 383

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(383)

<223> 5' terminal sequence. protein kinase c  
substrate 80 k-h (PRKCSH) gene.

&lt;400&gt; 263

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agttcgagga ggccgagcgg tcgctgaagg acatggagga gtccatcagg aacctggnag 180
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gcccgacca cnacaatttc agt 383

```

&lt;210&gt; 264

&lt;211&gt; 2056

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2056)

<223> protein kinase c substrate 80k -h (PRKCSH)  
gene.

&lt;400&gt; 264

```

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atgtgatccc ccacc                                     2056

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&lt;210&gt; 265

&lt;211&gt; 379

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence :primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(379)

<223> 5' terminal sequence. diphtheria toxin  
receptor (heparin-binding epidermal growth  
factor-like growth factor) (DTR) gene.

&lt;400&gt; 265

```

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aactcctgnc attcttctg                                     379

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&lt;210&gt; 266

&lt;211&gt; 2360

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2360)

<223> diphtheria toxin receptor (heparin-binding  
epidermal growth factor-like growth factor) (DTR)  
gene.

&lt;400&gt; 266

```

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&lt;210&gt; 267

&lt;211&gt; 435

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(435)

&lt;223&gt; 5' terminal sequence. integrin, beta 2

(antigen cd18 (p95), lymphocyte

function-associated antigen 1; macrophage antigen

1 (mac-1) beta subunit) (ITGB2) gene.

&lt;400&gt; 267

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aggagtcccc cggctgcccc tcaccctgtg gcaagtacat ctctgcgcc gagtgctga 60

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ccctttttca agagc 435

<210> 268

<211> 2776

<212> DNA/RNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(2776)

<223> integrin, beta 2 (antigen cd18 (p95),  
lymphocyte function-associated antigen 1;  
macrophage antigen 1 (mac-1) beta subunit) (ITGB2)  
gene.

<400> 268

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ctgccgttcg tgaacacgca ccctgataag ctgcgaaacc catgccccaa caaggagaaa 660  
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gtgaagggca ggacctgcaa ggagagggac tcagagggct gctgggtggc ctacacgctg 2100



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gagcagcagg acgggatgga ccgctacctc atctatgtgg atgagagccg agagtgtgtg 2160
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aaaataaaac ttcaat 2776

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&lt;210&gt; 269

&lt;211&gt; 449

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(449)

<223> 5' terminal sequence. neogenin (chicken)  
homolog 1 (NEO1) gene.

&lt;400&gt; 269

```

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tctagggaag ggagccggcc tccatgcca gtggttgctt ccagtgcctc t gaagtgcag 300
ggagaccaca aggtgtttg gaaggattnc gagagtaggt attgaaccag ntgaggttga 360
ncaaagagtt ggccatngg ggaaggattt aattgaangg gaccttaaac gtttttnac 420
aacagcttga cggactttta acggggggc 449

```

&lt;210&gt; 270

&lt;211&gt; 5297

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(5297)

&lt;223&gt; neogenin (chicken) homolog 1 (NEO1) gene.

&lt;400&gt; 270

```

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tctggtggag ccgtgggata cactctcagt tagaggctct tctgttatat taaactgttc 360
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```

gcattccaaa cacaataa ac ctgatgaagg ttattatcag tgtgtggcca ctgttgagag 540  
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aaaaaaaaa aaaaaaa 5297

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&lt;210&gt; 271

&lt;211&gt; 389

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(389)

<223> 3' terminal sequence. pou domain, class 2,  
transcription factor 2 (POU2F2) gene.

&lt;400&gt; 271

```

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aggaggttga cagggttgag gagggacttg tgagagctag aacttgga aatggcctag 180
cccacccttc aaaggggaaa agagggagga acaggggatg aaaagttntc cgcagccttc 240
ccttgaactc tcccctgctg ggggagggag gaggttaaag caagacccc tgcccaggtg 300
gggagagctg ggggccaggg gagaagggga caaatggtag ggacacattc tgtttgagca 360
caatgctaaa aattctgtac atcctttgg 389

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&lt;210&gt; 272

&lt;211&gt; 2048

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2048)

<223> pou domain, class 2, transcription factor 2  
(POU2F2) gene.

&lt;400&gt; 272

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```

cgtaacatg agttgggctt ggggcagatg aggtctggctg gcggggcggg cagcatggtt 60
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tgaaaaaaca acaaaaaaa ccaaaaaaa accaaaaaa aaaaaaaacc tctacccct 2040
ctagagcc 2048

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&lt;210&gt; 273

&lt;211&gt; 472

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(472)

<223> 3' terminal sequence. baculoviral iap  
repeat-containing 4 (BIRC4) gene.

&lt;400&gt; 273

```

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gaaattcaaa gatttatatt ccaactaaaa cactgccatg tacatTTTTT ttcctacttg 360
gtagcaaatg ctaatggaat tcaatcctga ttacttaaag tcagttcaca tcacacattc 420
aatcagggta ataagaacaa cataacatgc ctaccataga gttagatta a ga 472

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<210> 274  
<211> 2540  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(2540)  
<223> baculoviral iap repeat -containing 4 (BIRC4)  
gene.

<400> 274  
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ttaaaaactt ttgctaattt tccaagtggg agtcctgttt cagcatcaac actggcacga 180  
gcagggtttc tttatactgg tgaaggagat accgtgcggg gcttt agttg tcatgcagct 240  
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atccagaatg gtcagtcaca agttgaaaac tatctgggaa gcagagatca ttttgcctta 420  
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tttcagaact ggccagacta tgctcaccta accccaagag agttagcaag tgctggactc 600  
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gaggggccct ttacatttcg acttttttca ttttgttctg ttcggatttt ttataagtat 2400  
gtagaccccg aagggtttta tgggaactaa catcagtaac ctaacccccg tgactatcct 2460  
gtgctcttcc tagggagctg tgttgtttcc caccaccac ccttccctct gaacaaatgc 2520  
ctgagtgtcg gggcactttg 2540

181/292

<210> 275  
<211> 842  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(842)  
<223> 3' terminal sequence. death associated  
protein 3 (DAP3) gene.

<400> 275  
tagaaagata ttttattttt taggaaaaga gccataatta tcttaaa tgt gaaaaaccac 60  
atccaataaa ctgatataaa gttttaggaa caagggaata tcttattgtc acgcattcac 120  
agtgaaaacc attttaatgc aggtccagag ccaactgcag tcctgtccaa tcccataggt 180  
acaaggcct ggctcctctt cctgtgtact gcccgacttc ctcactttac tgggtccagc 240  
ataaagcaga tgtccactgt cttcct caca tgctgtgatc ttggcttaga ggtaggcaca 300  
gtgccgtcc agcagcgagg ggttcgcgtt acttaggaac agcagctctt tttcccttc 360  
ttctgtagga gctntctcat gttgaagcca attgttttcc aaataatact gaatacaact 420  
ttcaaatcc tttgggttat agttggaac caggatggga ataaagggat ccagggcac 480  
aaatccttc tttccagca actcctgcgg cagataggct ttccggggct taaagagaga 540  
cccagtctgg ctcagagcgg acacaatggc gcctccatgc caatcatnct tcatcatttt 600  
cctcagttgt gaacaagtgc taattccctc ggggcaatcg ggctttatct tctgttttca 660  
gagggttctt cccaangag cattgatgcc accacggcca cctatg ggtg aaacataccc 720  
caatgaactt tgctctttag ctctttcagc acaatttcaa actgatctgg tgcgtccctc 780  
aaccgtgtta tgccctgtca aaccacttct cccagaagac tccctttctt aggtttttct 840  
ct 842

<210> 276  
<211> 1608  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(1608)  
<223> death associated protein 3 (DAP3) gene.

<400> 276  
gaattccgcc ggccccaggc agcgtgtgtc ggtcgcctag gctggagaac tagtcct cga 60  
ctcacgtgca aggatgatgc tgaaaggaat aacaaggctt atctctagga tccataagtt 120  
ggacctggg cgttttttac acatggggac ccaggctcgc caaagcattg ctgctcacct 180  
agataaccag gttccagttg agagtccgag agctatttcc cgcaccaatg agaatgaccc 240  
ggccaagcat ggggatcagc acgaggttca gcaact caac atctccccc aggatttgga 300  
gactgtattt ccccatggcc ttctcctcgc ctttgtgatg cagggtgaaga cattcagtga 360  
agcttgccctg atggtaaagga aaccagccct agaacttctg cattacctga aaaacaccag 420  
ttttgcttat ccagctatac gatatttct gtatggagag aagggaacag gaaaaacct 480  
aagtctttgc catgttattc atttctgtgc aaaacaggac tggctgatac tacatattcc 540  
agatgctcat ctttgggtga aaaattgtcg ggtcttctg cagtccagct acaacaaca 600  
gcgctttgat caacctttag aggttcaac ctggctgaag aatttcaaaa ctacaaatga 660  
gcgcttctg caacagataa aagttcaaga gaagtatgtc tggaataaga gagaaa gcac 720  
tgagaaagg agtctcttg gagaagtgg tgaacagggc ataacacggg tgaggaaacgc 780  
cacagatgca gttggaattg tgctgaaaga gctaaaggag caaagttctt tgggtatgtt 840  
tcacctcta gtggccgtgg atggaatcaa tgctctttg ggaagaacca ctctgaaaag 900

182/292

```

agaagataaa agcccgattg ccccgagga atta gcactt gttcacaact tgaggaaaat 960
gatgaaaaat gattggcatg gaggcgcat tgtgtcggct ttgagccaga ctgggtctct 1020
ctttaagccc cgaaagcct atctgcccc ggagttgctg ggaaaggaag gatttgatgc 1080
cctggatccc ttattccca tcctggtttc caactataac ccaaaggaat ttgaaagttg 1140
tattcagtat tatttgga acaattggct tcaacatgag aaagctccta cagaagaagg 1200
gaaaaaagag ctgctgttcc taagtaacgc gaaccctcgc ctgctggagc ggcactgtgc 1260
ctacctctaa gccaagatca cagcatgtga ggaagacagt ggacatctgc tttatgctgg 1320
accagtaag atgaggaagt cgggcagtac acaggaagag gagccaggc c cttgtacct 1380
tggttgga caggactgca gttggctctg gacctgcatt aaaatgggtt tcaactgtga 1440
tgctgacaa taagatatc cctgttctt aaaactttat atcagtttat tggatgtggt 1500
ttttcacatt taagataatt atggctctt tcctaaaaaa taaaatatct ttctaaaaaa 1560
aaaaaaaaa aaaaaaaaaa aaa aaaaaaa aaaaaaaaaa aaaaaaa 1608

```

&lt;210&gt; 277

&lt;211&gt; 361

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(361)

<223> 5' terminal sequence. gonadotropin -releasing hormone 1 (leutinizing -releasing hormone) (GNRH1) gene.

&lt;400&gt; 277

```

ttagattgca tgctattgta tgtctacagg gcatttgaca gcccaggt aaatccaggt 60
gggacgggat ctaatgatgt cctgtccttc actgtccttg ccaccaccag ccacagagat 120
ccaggctttg gggactccca cagcttatcg accag tgttt gatttagttt ttagcctctt 180
tcccatcaaa tgaaaattaa cttggagaca catttcatta gaaaattaga ggcccccttg 240
gctaggaagg catctggtct ggggactaac tactttgaac agtgttgagt cctctctccc 300
acagatgggt cagccagcag taatgctnag ggaagactga agggatcaaa taganaaatg 360
t 361

```

&lt;210&gt; 278

&lt;211&gt; 470

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(470)

<223> gonadotropin-releasing hormone 1 (leutinizing -releasing hormone) (GNRH1) gene.

&lt;400&gt; 278

```

gggatctttt tggtctcttg cctctaaca gaatgaagcc aattcaaaaa ctctagctg 60
gccttattct actgacttgg tgctggaag gctgtccag ccagcactgg tcctatggac 120
tgcgccctgg aggaagaga gatgccgaaa atttgattga ttctttcca a gagatagtca 180
aagaggttgg tcaactggca gaaacccaac gcttcgaatg caccacgcac cagccacgtt 240
ctccctccg agacctgaaa ggagctctgg aaagtctgat tgaagaggaa actgggcaga 300
agaagattta aatccattgg gccagaagga atgaccatta ctaacatgac ttaagtataa 360
ttctgacatt gaaaatttat aacccat taa atacctgtaa atggtatgaa tttcagaaat 420

```

ccttacacca agttgcacat attccataat aaagtgtgtg gttgtgaatg

470

&lt;210&gt; 279

&lt;211&gt; 320

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(320)

<223> 3' terminal sequence. interleukin 2  
receptor, gamma (severe combined immunodeficiency)  
(IL2RG) gene.

&lt;400&gt; 279

ntctaaatat caacagaaac tttatttctc atcggttcag gaacaatcgg agggtagatg 60  
gaaagaggaa gggagggaaa gagggaggga ggaagaatcc tgcgaaaagg aagggccaga 120  
ctgagggaga agaaaaacat gttcggggca aaagggtaat tctcaagtgg ggaatgccaa 180  
atgaaggggt gcttacatgg gggcacaaaa ttccaaatca gccacagtgg ggtgaggtga 240  
gtatgagacg caggtggggt tgaatgaagg aaagttagta ccncttaggg ctacaggacc 300  
ctggggttct tctttcagag 320

&lt;210&gt; 280

&lt;211&gt; 407

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(407)

<223> 5' terminal sequence. interleukin 2  
receptor, gamma (severe combined immunodeficiency)  
(IL2RG) gene.

&lt;400&gt; 280

attcggcaca gggaactttt cggcctggag tgggtgtgtct aagggactgg ctgagagtct 60  
gcagccagac tacagtgaac gactctgcct cgtcagttag attcccccaa aaggaggggc 120  
ccttggggag gggcctgggc tncccoatgc aaccagcata gccctactg ggcccccca 180  
tgttacacc taaagcctga aacctgaacc ccantactct gacagaagaa cccaggggc 240  
ctgtagccct aagtggtagt aactttcctt cattcaacc acctgcgtct tatactcanc 300  
tcancacct gttggctgat ttggatttt tgtggcccca tgtaaggaac cttttaattt 360  
ggcattnccc aattgagaat taacctttt gnccgaaca tgttttt 407

&lt;210&gt; 281

&lt;211&gt; 1451

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;



<221> misc\_feature  
<222> (1)..(1451)  
<223> interleukin 2 receptor, gamma (severe  
combined immunodeficiency) (IL2RG) gene.

<400> 281

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gaagagcaag cgccatgttg aagccatcat taccattcac atccctctta ttctgcagc 60
tgcacctgct gggagtggg ctgaacacga caattctgac gcccaatggg aatgaagaca 120
ccacagctga tttcttcttg accactatgc ccactgactc cc tcagtgtt tccactctgc 180
ccctcccaga ggttcagtgt tttgtgttca atgtcgagta catgaattgc acttgggaaca 240
gcagctctga gccccagcct accaacctca ctctgcatta ttggtacaag aactcggata 300
atgataaagt ccagaagtgc agccactatc tattctctga agaaatcact tctggctgtc 360
agttgcaaaa aaaggagatc cacctctacc aaacatttgt tgttcagctc caggaccac 420
gggaacccag gagacaggcc acacagatgc taaaactgca gaatctggtg atccctggg 480
ctccagagaa cctaacactt cacaactga gtgaatccca gctagaactg aactggaaca 540
acagattctt gaaccactgt ttggagcact tgggtgcagta ccggactgac tgggaccaca 60 0
gctggactga acaatcagtg gattatagac ataagttctc cttgcctagt gtggatgggc 660
agaaacgcta cacgtttcgt gttcggagcc gctttaaccc actctgtgga agtgcctcagc 720
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tcctgtttgc attggaagcc gtggttatct ctgttggtc catgggattg attatcagcc 840
ttctctgtgt gtatttctgg ctggaacgga cgatgccccg aattcccacc ctgaagaacc 900
tagaggatct tgttactgaa taccacggga acttttcggc ctggagtggg gtgtctaagg 960
gactggctga gagtctgcag ccagactaca gtgaacgact ctgcctcgtc agtgagattc 1020
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cctactgggc cccccatgt tacaccctaa agcctgaaac ctgaacccca atcctctgac 1140
agaagaaccc cagggtcctg tagccctaag tggactaac tttccttcat tcaacccacc 1200
tgctgtctat actcacctca cccactgtg gctgatttg aattttgtgc cccatg taa 1260
gcaccccttc atttggcatt cccacttga gaattaccct ttgccccga acatgttttt 1320
cttctccctc agtctggccc ttcttttctg caggattctt cctccctccc tctttccctc 1380
ccttctctt tccatctacc ctccgattgt tcctgaaccg atgagaaata aagtttctgt 1440
tgataatcat c 1451
```

<210> 282

<211> 317

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(317)

<223> 3' terminal sequence. death associated  
protein 3 (DAP3) gene.

<400> 282

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atctaacaca acactttaga aagatatttt attttttagg aaaagagcca taattatctt 60
aaatgtgaaa aaccacatcc aataaactga tataaagttt taggnacaag ggaatatctt 120
attgtcacgc attcacagtg aaacccattt taatgcaggc ccagagccaa ctgcagtcct 180
gtccaatccc ataggggtaca agggcctggg ctctcttccc tgtgtactgc ccgacttcct 240
catcttactg gggccagca taaagcagga tgtccactgt ctctctcaca tgctgtganc 300
ttggncttag gaggtag 317
```

<210> 283

<211> 358

<212> DNA

<213> Artificial Sequence

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<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(358)  
<223> 5' terminal sequence. death associated  
protein 3 (DAP3) gene.

<400> 283  
aggacgggcg ctttggagcc ggccccaggc agcgtgtgtc ggtcgcctag tctggagaac 60  
tagtcctcga ctcacgtgca aggatgatgc tgaaaggaat aacaaggctt atctctagga 120  
tccataagtt ggacctggg cgttttttac acatggggac ccaggctcgn caaagcattg 180  
ctgctcacct agataaccca gttcccagt tgagagtccc gagagctatt ttcccgcaac 240  
caatgagaat gaccccggcc caagcatggg ggatcancaa ggagggtcaa gcaa tnacaa 300  
canttttccc cccaggattt tgggagaatt gtaattttcc ccatnggcct ttncttcc 358

<210> 284  
<211> 416  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(416)  
<223> 5' terminal sequence. ptk2 protein tyrosine  
kinase 2 (PTK2) gene.

<400> 284  
gcacagaagc tattgaactc tgacctgggt gagctcatca acaagatgaa actggcccag 60  
cagtatgtca tgaccagcct ccagcaagag tacaaaaagc aaatgctgac tgctgctcac 120  
gccctggctg tggatgccaa aaacttactc gatgtcattg a ccaagcaag actgaaaatg 180  
cttgggcaga cgagaccaca ctgagcctcc cctaggagca cgtcttgcta ccctcttttg 240  
aagatgttct ctagccttcc accagcagcg agganttaac cctgtgtcct cagtncgcca 300  
gcacttacag ctccaacttt tttgaatgac catctggttg aaaaatcttt ctcataataag 360  
tttnaaccac atttggattt ggggttcatt ttttgttttg ttttttttc aatcat 416

<210> 285  
<211> 3052  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(3052)  
<223> ptk2 protein tyrosine kinase 2 (PTK2) gene.

<400> 285  
ccggtgtgaa ggccatgagt gattactggg ttgttggaag gaagtctaac tatgaagtat 60  
tagaaaaaga tgttggttta aagcgatttt ttctaagag tttactggat tctgtcaagg 120  
ccaaaacact aagaaaactg atccaacaaa catttagaca atttgccaac cttaatagag 180  
aagaaagtat tctgaaattc tttgagat cc tgtctccagt ctacagattt gataaggaat 240  
gcttcaagtg tgctcttggg tcaagctgga ttatttcagt ggaactggca atcgccccag 300

186/292

```

aagaaggaat cagttaccta acggacaagg gctgcaatcc cacacatctt gctgacttca 360
ctcaagtgc aaccattcag tattcaaaca gtgaagacaa ggacagaaaa ggaatgctac 420
aactaaaaat agcagggtgca cccgagcctc tgacagtgc ggcaccatcc ctaaccattg 480
cggagaatat ggctgacctc atagatgggt actgccggct ggtgaatgga acctcgagc 540
catttatcat cagacctcag aaagaagggt aacggggcttt gccatcaata ccaaagtgg 600
ccaacagcga aaagcaaggc atcgcgacac acgcggtctc tgtgtcag aa acagatgatt 660
atgctgagat tatagatgaa gaagatactt acaccatgcc ctcaaccagg gattatgaga 720
ttcaaaagaga aagaatagaa cttggacgat gtattggaga aggccaatTT ggagatgtac 780
atcaaggcat ttatatgagt ccagagaatc cagctttggc ggttgcaatt aaaacatgta 840
aaaactgtac ttcgagacgc gtgaga gaga aatttcttca agaagcctgc cattacacat 900
ctttgcactg gaattgggtgc agatatataa gtgataccta tgttgatgcc tgcccagacc 960
ccaggaatgc agagttaaca atgcgtcagt ttgaccatcc tcatattgtg aagctgattg 1020
gagtcacac agagaatcct gtctggataa tcatggagct gtgcacactt ggagagctga 1080
ggtcattttt gcaagtaagg aaatacagtt tggatctagc atctttgatc ctgtatgcct 1140
atcagcttag tacagctctt gcatactag agagcaaaag atttgtacac agggacattg 1200
ctgctcgga tgttctgggt tcctcaaagt attgtgtaaa attaggagac tttggattat 1260
ccgatatat ggaagatagt acttactaca aagcttccaa a ggaattg cctattaaat 1320
ggatggctcc agagtcaatc aattttcgac gttttacctc agctagtgc gtatggatgt 1380
ttgggtgtgt tatgtgggag atactgatgc atggtgtgaa gccttttcaa ggagtgaaga 1440
acaatgatgt aatcggtcga attgaaaatg gggaaagatt accaatgcct ccaaattgtc 1500
ctcctaccct ctacagcctt atgacgaaat gctgggccta tgacccagc aggcggccca 1560
ggttttactga acttaagct cagctcagca caatcctgga ggaagagaag gctcagcaag 1620
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gattttatcc cagcccacag cacatggtac aaaccaatca ttaccagggt tctggctacc 1800
ctggttcaca tggaatcaca gccatggctg gcagcatcta tccagggtcag gcattctctt 1860
tggaccaaac agattcatgg aatcatagat ctcaggagat agcaatgtgg cagcccaatg 1920
tggaggactc tacagtattg gacctgcgag ggattgggca agtgttgcca acccatctga 1980
tggaagagcg tctaaccga cagcaacagg aaatggaaga agatcagcgc tggctggaaa 2040
aagaggaaa atttctgatt ggaaccaaac atatatatca gcctgtgggt aaaccagatc 2100
ctgcagctcc accaaagaaa ccgcctcgcc ctggagctcc cggtcactct ggaagccttg 2160
ccagcctcag cagccctgct gacagctaca acgaggggtg caagcttcag cccagggaaa 2220
tcagccccc tcctactgcc aacctggacc ggtcgaatga taagggtgtac gagaatgtga 2280
cgggctgggt gaaagctgtc atcgagatgt ccagtaaaat ccagccagcc ccaccagagg 2340
agtatgtccc tatggtgaag gaagtgggt tggccctgag gac attattg gccactgtgg 2400
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tattgaactc tgacctgggt gagctcatca acaagatgaa actggcccag cagtatgtca 2520
tgaccagcct ccagcaagag taaaaaagc aaatgctgac tgccgctcac gccctggctg 2580
tggatgcaa aaacttac tc gatgtcattg accaagcaag actgaaaatg ctggggcaga 2640
cgagaccaca ctgagcctcc cctaggagca cgtcttgcta ccctcttttg aagatgttct 2700
ctagccttcc accagcagc aggaattaac cctgtgtcct cagtogccag cactcacagc 2760
tccaactttt ttgaatgacc atctggttga aaaatctttc tcatataagt ttaacca cac 2820
tttgatttgg gttcattttt tgttttgtt ttttcaatca tgatattcag aaaaatccag 2880
gatccaaaat gtggcgtttt tctaagaatg aaaattatat gtaagctttt aagcatcatg 2940
aagaacaatt tatgttcaca ttaagatacg ttctaaaggg ggatggccaa ggggtgacat 3000
cttaattcct aaactacctt agctgcatag t ggaagagga gagccggaat tc 3052

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&lt;210&gt; 286

&lt;211&gt; 377

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(377)

<223> 3' terminal sequence. cyclin -dependent  
kinase 4 (CDK4) gene.

&lt;400&gt; 286

```
gnataaaaaa ggaccccaaa tataaaggna gggaaaggga caagaggga cataccctt 60
agtgtagaga aatgggaagg agaaggagaa gcctcaaaag gaggtgggag gggaatgtca 120
ttaaggcagc aaagtaatct ctgtagaaag atggaggagg accctccata gcctcagaga 180
taaaggcaaa gattgccctc tc agtgtcca gaagggaat gggcagcttt tcttcntcc 240
atgggcagcc actccattgc tccctccggn ttaccttcac cttatgtag gataagagtn 300
ctgcagagct tcgaaagggc agagattcgc ttgtgtggg ttaaaagtca gcatttccan 360
cagcagcttt tgcttcc 377
```

&lt;210&gt; 287

&lt;211&gt; 363

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(363)

<223> 5' terminal sequence. cyclin -dependent  
kinase 4 (CDK4) gene.

&lt;400&gt; 287

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catatctgga caaggcacc ccaccaggt tgcagccga acgatcaagg atctgatgcg 60
ccagtttcta agaggcctag atttccttca tgccaattgc atcggtcacc gagatctgaa 120
gccagagaac attctggtga caagtgtng aacagtcaag ctggctgact ttngcctggc 180
cagaatctac agctaccaga tggcacttac acccgtggtt gttacactct ggtacc gagg 240
tcccgaagtt cttctngcag tccacatatg caacacctgt gggacatgtg ggagtgttg 300
ctgtatcttt gcagagatgt ttctgcgaaa ncctctcttt ctgtggnaaa ctctgtaagg 360
ccg 363
```

&lt;210&gt; 288

&lt;211&gt; 1443

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1443)

&lt;223&gt; cyclin-dependent kinase 4 (CDK4) gene.

&lt;400&gt; 288

```
gccctcccag tttccgcgcg cctctttggc agctggtcac atggtgaggg tgggggtgag 60
ggggcctctc tagcttgccg cctgtgtcta tggcggggcc ctctgcgtcc agctgctccg 120
gaccgagctc ggggtgatgg ggcgtagga accggctccg gggccccgat aacgggccgc 180
ccccacagca ccccgggctg gcgtgagggt ctcccttgat ctgagaatgg ctacctctcg 240
atatgagcca gtggctgaaa ttggtgtcgg tgcctatggg acagtgt aca agggccgtga 300
tcccacagt ggccactttg tggccctcaa gagtgtgaga gtcccaatg gaggaggagg 360
tggaggaggc cttcccatca gcacagttcg tgagggtggc ttactgaggc gactggaggc 420
ttttgagcat cccaatgttg tccggctgat ggacgtctgt gccacatccc gaactgaccg 480
ggagatcaag gtaaccctgg tgttt gagca tgtagaccag gacctaagga catatctgga 540
caaggcacc ccaccaggt tgcagccga aacgatcaag gatctgatgc gccagtttct 600
aagggccta gatttccttc atgccaattg catcggtcac cgagatctga agccagagaa 660
cattctggtg acaagtggtg gaacagtcaa gctggctgac tttggcctgg ccagaatcta 720
```

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```

cagctaccag atggcactta caccctgtgt tggtacactc tggtagcgag ctcccgaagt 780
tcttctgcag tccacatatg caacacctgt ggacatgtgg agtggttggt gtatctttgc 840
agagatgttt cgtcgaaagc ctctcttctg tggaaactct gaagccgacc agttgggcaa 900
aatctttgac ctgattgggc tgcctccaga ggatgactgg cctcg agatg tatccctgcc 960
ccgtggagcc tttcccccca gagggccccg cccagtgcag tgggtgttac ctgagatgga 1020
ggagtcggga gcacagctgc tgcctgaaat gctgactttt aaccacaca agcgaatctc 1080
tgcctttcga gctctgcagc actcttatct acataaggat gaaggtaatc cggagtgagc 1140
aatggagtgg ctgccatgga aggaagaaaa gctgccattt cccttctgga cactgagagg 1200
gcaatctttg cctttatctc tgaggctatg gagggctctc ctccatcttt ctacagagat 1260
tactttgctg ccttaatgac attcccctcc cacctctcct tttgaggctt ctcttctcc 1320
ttccatttc tctacactaa ggggtatgtt ccctcttgct cctttcccta cctttatatt 1380
tggggtcctt ttttatacag gaaaaacaaa accaaaagaa awaatggccc tttttttttt 1440
ttt 1443

```

&lt;210&gt; 289

&lt;211&gt; 394

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(394)

<223> 3' terminal sequence. basic transcription  
factor 3 (BTF3) gene.

&lt;400&gt; 289

```

cccgcgtgtg tgcgcctaan ctgagnggn ccacccgaga ccccttgagc accaacccta 60
gtccccgcg cggccctna ttcgctccga caagatgaaa gaaaca atca tgaaccagg 120
aaaactcgcc aaactgcagg cacaagtgcg cattggtggg aaaggaactg ctgcagaaa 180
gaagaagggt gttcatagaa cagccacagc agatgacaaa aaacttcagt tctccttaa 240
gangttagg gtaaacata tctctggnat tgaagagggt aatatgttta caaaccagg 300
aacagtgatc cactttaaca acc tnaagt tcagggcatc tctgggcagc ggacactttc 360
accattacng gccttgctga gncaaagcag ctgg 394

```

&lt;210&gt; 290

&lt;211&gt; 477

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(477)

&lt;223&gt; basic transcription factor 3 (BTF3) gene.

&lt;400&gt; 290

```

atgcgacgga caggcgacc cgctcaggct gactctcggg ggcgaggctg agccaggggc 60
ggctgcctg gggcgaggc gacgctgtct caacctccac ctgcggcg g aaccgagga 120
gaggagcctc agatgaaaga aacaatcatg aaccag gaaa aactcgccaa actgcaggca 180
caagtgcgca ttggtgggaa agtgaatatg ttacaaaacc aaggaacagt gatccacttt 240
aacaacccta aagttcaggc atctctggca gcgaacactt tcaccattac aggccatgct 300
gagacaaagc agctgacaga aatgctaccc agcatcttaa accagcttgg tgcggatagt 360
ctgactagtt taaggagact ggccgaagct ctgccaaaac aatctgtgga tggaaaagca 420
ccatttgcta ctggagagga tgatgatgat gaagttccag gaggttcca agaata 477

```

<210> 291  
<211> 388  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(388)  
<223> 3' terminal sequence. colony stimulating  
factor 1 receptor, formerly mcdonough feline  
sarcoma viral (v-fms) oncogene homolog (CSF1R)  
gene.

<400> 291  
tgctgttagt ttaatgtgga cagagacatc ccacggcgtg actgttagt t aggatgagtc 60  
agcttggggg agtttgtgct tcctgcttgg nggtggccagc cacatgccaa ggtcccctgc 120  
cttctagccc agaatgacgg gactgggcag aacacccccca acttttagct gccacttggc 180  
tcattacagc agtaccagta tgggggtggg aggggtgagg cnttggagtg aaggcggcgt 240  
atagggcaga gactaagagg gtcctgtg ag attccttagag gagccatcct gntccaaggg 300  
gcctgagctg agtntgggtc tgtgagcatc tgctgtcct ctcagagagg ggagatctca 360  
ctctctgccg gtctgtctag ccccaaag 388

<210> 292  
<211> 3992  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(3992)  
<223> colony stimulating factor 1 receptor,  
formerly mcdonough feline sarcoma viral (v-fms)  
oncogene homolog (CSF1R) gene.

<400> 292  
ggcttcagga agggcagaca gagtgtccaa aagcgtgaga gcacgaagtg aggagaaggt 60  
ggagaagaga gaagaggaag aggaagagga agagaggaag cggaggggaac tgcggccagg 120  
ctaaaagggg aagaagagga tcagcccaag gaggaggaag aggaaaacaa gacaaacagc 180  
cagtgcagag gagaggaacg tgtgtccagt gtcccgatcc ctgcggagct agtagctgag 24 0  
agctctgtgc cctgggcacc ttgcagccct gcacctgcct gccacttccc caccgaggcc 300  
atgggcccag gagttctgct gtcctgctg gtggccacag cttggcatgg tcagggaatc 360  
ccagtgatag agcccagtgt ccccgagctg gtcgtgaagc caggagcaac ggtgaccttg 420  
cgatgtgtgg gcaatggcag cgtggaatgg gatggccccg catcacctca ctggaccctg 480  
tactctgatg gctccagcag catcctcagc accaacaacg ctaccttcca aaacacgggg 540  
acctatcgct gcactgagcc tggagacccc ctgggaggca gcgcggccat ccacctctat 600  
gtcaaagacc ctgcccggcc ctggaacgtg ctagcacagg aggtggtcgt gttcagaggac 660  
caggacgcac tactgccctg tctgtctaca gaccgggtgc tggaaagcagg cgtctcgctg 720  
gtgcgtgtgc gtggcgggcc cctcatgcgc cacaccaact actccttctc gccctggcat 780  
ggcttcacca tccacagggc caagttcatt cagagccagg actatcaatg cagtgccttg 840  
atgggtggca ggaaggtgat gtccatcagc atccggctga aagtgcagaa agtcatccca 900  
gggccccag ccttgacact ggtgcctgca gagctgggtc ggattcgagg ggaggctgcc 960  
cagatcgtgt gtcagccag cagcgttgat gttactttg atgtcttcct ccaacacaac 1020

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aacactaagc tcgcaatccc tcaacaatct gactttcata ataaccgtta ccaaaaagtc 1080
ctgacctca acctcgatca agtagatttc caacatg ccg gcaactactc ctgcgtggcc 1140
agcaacgtgc agggcaagca ctccacctcc atgtttctcc ggggtgtaga gagtgcctac 1200
ttgaacttga gctctgagca gaacctcatc caggaggtga ccgtggggga ggggtcaac 1260
ctcaaagtca tgggtggaggc ctaccaggc ctgcaagggt ttaactggac ctacctggga 1320
cccttttctg accaccagcc tgagcccaag ctgtgtaatg ctaccacca ggacacatac 1380
aggcacacct tcacctctc tctgccccgc ctgaagccct ctgaggctgg ccgctactcc 1440
ttcctggcca gaaaccagg aggttgaga gctctgacgt ttgagctcac ccttcgatac 1500
ccccagagg taagcgtcat atggacattc atcaacggct ctggcacctc tttgtgtgct 1560
gcctctgggt accccagcc caacgtgaca tggtcgagc gcagtggcca cactgatagg 1620
tgtgatgagg cccaagtgtc gcaggtctgg gatgacccat accctgaggt cctgagccag 1680
gagcccttcc acaaggtagc ggtgcagagc ctgctgactg ttgagacctt agagcacaac 1740
caaacctacg agtgcagggc ccaca acagc ctggggagtg gctcctgggc cttcataccc 1800
atctctgcag gagccacac gcatcccccg gatgagttcc tcttcacacc agtggtggtc 1860
gcctgcattg ccatcatggc cttgctgctg ctgctgctcc tgctgtatt gtacaagtat 1920
aagcagaagc ccaagtacca ggtccgctgg aagatcatcg agagctatga gggcaacagt 1980
tatactttca tcgacccac gcagctgctc tacaacgaga agtgggagtt ccccggaac 2040
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gcctttgtgc tgggcaagga ggatgctgct ggaaggtgg ctgtgaagat gctgaagtcc 2160
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aacatccacc tcgagaagaa atatgtccgc agggacagtg gcttctccag ccagggtgtg 2460
gacacctatg tggagatgag gcctgtctcc acttcttcaa atgactcctt ctctgagcaa 2520
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tggactgact ttatgcctat gaagtcccca ggagctacac tgatactgag aaaaccaggc 3600
tctttggggc tagacagact ggcagagagt gagatctccc tctctgagag gagcagcaga 3660
tgctcacaga ccacactcag ctcaggcccc ttggagcagg atggctcctc taag aatctc 3720
acaggacctc ttagtctctg cctatacgc cgccttact ccacagcctc acccctccca 3780
ccccatact ggtactgctg taatgagcca agtggcagct aaaagtggg ggtgtctgc 3840
ccagtcccgt cattctgggc tagaaggcag gggaccttgg cattggctgg ccacaccaag 3900
caggaagcac aaactcccc aagctgact c atcctaacta acagtcacgc cgtgggatgt 3960
ctctgtccac attaaactaa cagcattaat gc
3992

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&lt;210&gt; 293

&lt;211&gt; 356

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

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<221> misc\_feature  
 <222> (1)..(356)  
 <223> 3' terminal sequence. friend leukemia virus  
 integration 1 (FLI1) gene.

<400> 293  
 tttatttagt caaattattt tacaacatgg ncttctttga cagttgtcag cttaacactt 60  
 aatatagtta aaaaagtcaa caattacctg caaaattata tataatnnaa tgtctaaaaa 120  
 tatgtngctt atatagagca ggaaaatccc tctctccac aagggaaggt ttcgttggtt 180  
 tnccagagc tgtgattatn gcagtactgt tacacgcatt tccaaagcat taaagancta 240  
 aatgggatta tcttttncct gcttgtgtat gcctgtnaaa taactgtacc agtggctttg 300  
 ctttctcata ggtcagtgac ttaaacagcc ctgtttcctt ttcggctata g ggcatt 356

<210> 294  
 <211> 465  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(465)  
 <223> 5' terminal sequence. friend leukemia virus  
 integration 1 (FLI1) gene.

<400> 294  
 gaccaaagca gtttcttgtc aatacacggg gttcagtatg acacagaatc atggacttaa 60  
 cccgtcatgt tctggtttga gatattagtg caaatagagg tgggaagctt ataattctaat 120  
 tttaggagga ccaatttcag tggatggcaa ctggaacatt gattgtaagg ccagtgaagt 180  
 tttcacccaa ctggaatttg atggaaagaa ggtt tgtgtg tttaagacgc caagggcatt 240  
 gcagaatccc tctcagtga cagtatgcac tcagctgacc actctctcta gccaatagtc 300  
 aagatatgga actaaggaaa ttttaatgcc aaattacata cattcctgaa agacggggga 360  
 attaaattna ctaattttnt tttttttttt ttaaatgatn gacagtggtt ccccggaact 420  
 tgggaaangt tgtaggggnt ttctaaaccc aagncgattc gcant 465

<210> 295  
 <211> 2957  
 <212> DNA/RNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(2957)  
 <223> friend leukemia virus integrati on 1 (FLI1)  
 gene.

<400> 295  
 gaattcccaa acgtgcacag gggagtgagg gcagggcgct cgcagggggc acgcagggag 60  
 ggcccagggc gccagggagg ccgcgccggg ctaatccgaa ggggctgcga ggtcaggctg 120  
 taaccgggtc aatgtgtgga atattggggg gctcggctgc agacttgcc aaatggacgg 180  
 gactattaag gaggctctgt cgggtgtgag cgacgaccag tccctctttg actcagcgta 240  
 cggagcggca gccatctcc ccaaggccga catgactgcc toggggagtc ctgactacgg 300  
 gcagcccccac aagatcaacc ccctcccacc acagcaggag tggatcaatc agccagtgag 360  
 ggtcaacgtc aagcgggagt atgaccacat gaatggatcc agggagtctc c ggtggactg 420



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cagcgttagc aaatgcagca agctgggtggg cggaggcgag tccaacccca tgaactacaa 480
cagctatatg gacgagaaga atggccccc tcctcccaac atgaccacca acgagaggag 540
agtcacgtgc cccgcagacc ccacactgtg gacacaggag catgtgaggc aatggctgga 600
gtggggccata aaggagtaca gcttgatgga gatcgacaca tcctttttcc agaacatgga 660
tggcaaggaa ctgtgtaaaa tgaacaagga ggacttcctc cgcgccacca ccctctacaa 720
cacggaagtg ctgttgtcac acctcagtta cctcagggaa agttcactgc tggcctataa 780
tacaacctcc cacaccgacc aatcctcacg attgagtgtc aaagaagacc cttcttatga 840
ctcagtcaga agaggagctt ggggcaataa catgaattct ggctcaaca aaagtccctc 900
ccttggaagg gacaaaacga tcagtaagaa tacagagcaa cggccccagc cagatccgta 960
tcagatcctg ggcccagacca gcagtgcct agccaaccct ggaagcgggc agatccagct 1020
gtggcaattc ctctggagc tgctctccga cagcgccaac gccagctgt a tcacctggga 1080
ggggaccaac ggggagttca aaatgacgga cccgatgag gtggccaggc gctggggcga 1140
gcggaaaagc aagccaaca tgaattacga caagctgagc cgggccctcc gttattacta 1200
tgataaaaac attatgacca aagtgcacgg caaaagatat gcttacaat ttgacttcca 1260
cggcattgac caggctctgc agc cacatcc gaccgagtcg tccatgtaca agtacccttc 1320
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gacctcccc acggggggaa tctaccccaa cccaacgtc ccccgccatc ctaacaccca 15 00
cgtgccttca cacttaggca gctactacta gaagcttctt ctactgaag cccatcctgc 1560
acacttactg gatgctttgg actcaacagg acatattgtg ccttgaaggg aagacaaaac 1620
tggatgttct ttctgttgg atagaacctt tgtatttgtt ctttaaaaac atttttttta 1680
atgttggtaa ctttgcctc ctctacctga acaaaga gat gaataattcc atgggccagt 1740
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atggttaagt catggttctg agaaagaagc tgtacgtttt ctttatgttt ttatgaccaa 1860
agcagtttct tgtcaataca cggggttcag tatgacacag aatcatggac ttaaccgctc 1920
atgttctggt ttgagattta gtgacaaata gaggtgggaa gcttataatc taattttagg 1980
aggaccaaat tcagcggatg gcaactggaa cattgattgt aaggccagtg aagttttcac 2040
ccaactggaa ttgatggaa agaaggtttg tgtgtttaag acgccaaggg cattgcagaa 2100
tccctctcag tggacagtat gcactcagct gaccactctc tctagaaata gtcaagatat 2160
gaactaagaa attttaatgc aaatacatac attcctgaaa gacggggaat taaattacta 2220
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aaactcaagc agattcgcaa gtgtgtgctg cttgtcagac catcagacca gggccaacca 2340
atcagaaggc aacttactgt ataaa ttatg cagagttatt ttctatatc tcacagtatt 2400
aaaaaataaa taattaaaaa ttaagaataa ataaacgagt tgacctcggc caaaaagca 2460
gttttactat cgaatcaatc gctgttattt ttttttaag taatttgtag atcttttttc 2520
aatctgtaca tttgggctgt cttgtatgtt tttatgctcc tttttaaaaa gcataatatg 2580
cctatagctg aaaaaggaaac agggctgttt aagtcactga cttatgagaa agcaaagcac 2640
tggtacagtt atttaacagg catacacaag cagggaaaag ataatccatt tagatcttta 2700
atgctttgga aatgcgtgta acagtactgc aataatcaca gctctgggaa aaacaacgaa 2760
actttccctt gtggagagga gggattttcc tgctctata t aagcaacata tttttagaca 2820
ttaaaatata tataattttg caggttaattg ttgacttttt taactatatt aagtgttaag 2880
ctgacaactg tcaaagaaga coatgttgta aaataatttg actaaataaa tggttccttc 2940
tctcaaaaaa aaaaaaa 2957

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&lt;210&gt; 296

&lt;211&gt; 400

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(400)

<223> 3' terminal sequence. ests, highly similar  
to tvhume hepatocyte growth factor receptor  
precursor [h.sapiens] (EST R97218) gene.

&lt;400&gt; 296

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```
caccccttct cttcacagat cacgaagatc ccattgaatg gcttgggctg cagacatttc 60
cagtcctgca gtcaatgcct ctctgcccc ccctttgttc agtgtggctg gtgcaganca 120
aatgtgtgcg atcggaggaa tgcctgagcg ggacatggac tcaacagatc tgtctgcctg 180
caatctacaa ggtaggaatc tctaacagct ggcatacatg tttttgtttg gtgttttttt 240
tttttttttg gtttggtttg gtttggtttt tggtttttta gatacaaac ccactaatga 300
aaaaaattta aaaatcaatt tactcattta ggctgtgagg tcatcaggct aaagcaccat 360
ctctctcttg ggctttatcc ctggggcagg ggagggggg 400
```

&lt;210&gt; 297

&lt;211&gt; 464

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(464)

<223> 5' terminal sequence. ests, highly similar  
to tvhume hepatocyte growth factor receptor  
precursor [h.sapiens] (EST R97218) gene.

&lt;400&gt; 297

```
cgtgtagat tttcatagtg ccgaatatat gcttaagcaa ataaggcaac acagtttagca 60
tggctgcgat gttagccaat gtccattgcc agaaactgag ttctctatca gcaagagatg 120
tgctcatctt gttctggact atatctctc a gggactaga gggcagcctg ctaaattgga 180
tgcactcaat aaatatTTTT ggaatgaatt aaagagtggc atggcttaca gaagtataga 240
tgtagtata gtcatccgtt gagcctttgc ttttttttct gggaacactg aaggaagact 300
cacagccacc catgggtgtt tgacctcca cttgccttgc ccacctcacc ccgggaaata 360
atcttcagtc tcatctgtgg aacagacaag gccaccntct atggcttcgg nacaggtagn 420
aaaactgtcc tgtgtggccc cgctnggcag ggatcaccag tttg 464
```

&lt;210&gt; 298

&lt;211&gt; 378

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(378)

<223> 3' terminal sequence. ets variant gene 5  
(ets-related molecule) (ETV5) gene.

&lt;400&gt; 298

```
aaatacaaaa actacaaaaa tcagtttata aactgttttt ccaaaacaac caccaaaaaca 60
aaacaatccc ccaaatcagg gcaaaacaaa atactgtcaa aagtgttaat cgcccttctc 120
ctaaaataaa agtcatccac actcagccac gtgattggga agagaaaggg ggcttgctct 180
acttggcgac cacatggccg ggtggttccc aagagtagcc atggtttatg attttgagaa 240
ccacggaggg ggnaaacagc tgttctgact gcccccttt ttctagacaa ggggtaatat 300
ttcagattca gctagaagag ctttccaat g ttttaagatgt atttttaanc cttaatgggt 360
tnaggcctcc ccaacttt 378
```

&lt;210&gt; 299

&lt;211&gt; 317

194/292

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(317)

<223> 5' terminal sequence. ets variant gene 5  
(ets-related molecule) (ETV5) gene.

&lt;400&gt; 299

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ggataaccag cgtccgttcc tgaaggcaga gtccgagtgc cacctcagcg aggaggacac 240
cctgcgcgtg acccactttg aagacagccc cgcttacctc ctggacatgg accgctgcag 300
cagcctcccc tatgccg                                     317
```

&lt;210&gt; 300

&lt;211&gt; 4071

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(4071)

<223> ets variant gene 5 (ets -related molecule)  
(ETV5) gene.

&lt;400&gt; 300

```
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tgctgaaacc tctcaaagtg gtattagaga cgctgaaagc accatggacg ggttttatga 240
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195/292

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gctgcgttat attctgtact gtgtacaata aagaagttg cttttcgttt a 4071

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&lt;210&gt; 301

&lt;211&gt; 407

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(407)

<223> 3' terminal sequence. cyclin -dependent  
kinase 4 (CDK4) gene.

&lt;400&gt; 301

nccngtataa aaaaggaccc caaatataaa ggtagggaaa gggacaagag ggaacata cc 60

196/292

```

ccttagtgta gagaaatggg aaggagaagg agaagcctca aaaggngagg tgggagggga 120
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cagagntaaa ggcaaagntt gccctctcag tntccngaag ggaaatggca gcttttcttc 240
cttccatggg cagccactcc attgctcact cgggatt acc ttcacctta ttaggataa 300
gggtgctgca gagctcgaaa ggcagagat tcgcttntgt ggggttaaaa gtcagccttt 360
ncccgagca gctttgcttc cccgactcct nccttttcag gnacccc 407

```

&lt;210&gt; 302

&lt;211&gt; 405

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(405)

<223> 5' terminal sequence. cyclin -dependent  
kinase 4 (CDK4) gene.

&lt;400&gt; 302

```

attcgnaca gaggaggagg tggaggaggc cttcccatca gcacagtctg tgaggtggct 60
ttactgaggc gactggaggc ttttgagca t cccaatgttg tccggctgat ggacgtctgt 120
gccacatccc gaactgaccg ggagatcaag gtaaccctgg tgtttgagca ttagaccag 180
gacctaagga catatctgga caaggcacc ccaccaggct tgccagccga aacgatcaag 240
gatctgatgc gccagtttct aagaggccta gatttccttc atgccaattg catcgttcac 300
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ggactttggg cctgggcagn aatctancag cttaccagat gggca 405

```

&lt;210&gt; 303

&lt;211&gt; 420

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(420)

<223> 3' terminal sequence. v -yes-1 yamaguchi  
sarcoma viral oncogene homolog 1 (YES1) gene.

&lt;400&gt; 303

```

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ttaagtttag gctaccatta ttcatttaaa aaagtgtgct agaaggctgt ttttgccaac 120
ttcctttttt ggtaagggtt aacttccaca ttaagacact gaagacgaaa agctgttggt 180
aaaatatctc caaatttaca aagttgtttt tcttgggcaa tttaaaaata caggancaat 240
ttaaantgaa tacacattaa gtttaggtgt tttatcccta ctatacaatt gttattatat 300
agggaactgc tcccttcn gg ttaaanccct aatggaatac ccatcaactt ttcccggccc 360
ntactttccc nggattgggg tttagggtac ctaaacggga aatttaggtc nccccntttg 420

```

&lt;210&gt; 304

&lt;211&gt; 4517

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(4517)

<223> v-yes-1 yamaguchi sarcoma viral oncogene  
homolog 1 (YES1) gene.

&lt;400&gt; 304

```
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gtcgcctatc ctgaccacag caaagcggcc cggagcccg cggaggggacc tgacgggggc 120
gtaggcgccg gaagcgctgg gccccggag ccgggcccgc gtggcccgag ttccggtgag 180
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198/292

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&lt;210&gt; 305

&lt;211&gt; 459

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(459)

&lt;223&gt; 3' terminal sequence. interferon -induced protein 75, 52kd (IFI75) gene.

&lt;400&gt; 305

```

ncttgctga aggtgtgctg gacacctcct ggggctcttc tgggtcattt ggttctggag 60
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gcncaatngg gtatggaagg aagcttcct ctaanaagg 459

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&lt;210&gt; 306

&lt;211&gt; 370

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

199/292

<221> misc\_feature  
<222> (1)..(370)  
<223> 5' terminal sequence. interferon -induced  
protein 75, 52kd (IFI75) gene.

<400> 306  
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ctgtntctctt 370

<210> 307  
<211> 1541  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(1541)  
<223> interferon-induced protein 75, 52kd (IFI75)  
gene.

<400> 307  
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gtaactccac ggtagagaca agggcccaaa aggcgagaac tgaatgtgcc cgaaagtcga 600  
gatcagagga gatcattgat ggcacttcag aaatgaatga aggaaagagg tcccagaaga 660  
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aggtcatgat gaggttccaa aaggcaagaa ctaaatgtgc ccgaaagtcc agatcgaaag 840  
aaaagaaaaa ggagaaagat atctgttcaa gctcaaaaag gagatttcag aaaaatattc 900  
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tgagttcctc ctcttgaagg cctactgtca tccacaaagc tcctttttta cgg gcatccc 1440  
atttaatat cgagattacg gtgagccttt caggaagcaa tgtggttgga cctgggtaag 1500  
ggaaaggctg attacggaaa tgtacacggt ggcgccgaat t 1541

<210> 308  
<211> 416  
<212> DNA



200/292

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(416)

<223> 3' terminal sequence. v-myb avian  
myeloblastosis viral oncogene homolog -like 2  
(MYBL2) gene.

&lt;400&gt; 308

```
gttannncan tnnatTTTTT aagagagagg caattttatt cttccaaaaa aatgcaccag 60
agagggtgag cacaggagca cccctggcca catcccccat cctaagcagg gtctgagatg 120
aggccaggnc tgacgtgggc ttgggagaag ctgacggagc tcctgtggc cttggggagg 180
gaaccaggca gacctgggaa gtggaacttt gttgttagca ccaggagccg cccacagctg 240
ggcttcggca acagggcagc acatggccct gttccttcca cctgagagt c tggggagggg 300
ctggtggcag aaggctccct gcaggagggtt cacctgaatg actctcagat tcacagaccc 360
cctnttgccc ccacaacccc tgtaaaccatg agaatggggc tcgtgacacc ctnaac 416
```

&lt;210&gt; 309

&lt;211&gt; 426

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(426)

<223> 5' terminal sequence. v-myb avian  
myeloblastosis viral oncogene homolog -like 2  
(MYBL2) gene.

&lt;400&gt; 309

```
gaactcatca tcgaggacga catcaggccc gagaagcaga agaggaagcc tgggctgcgg 60
cggacccatt caagaaagtc cggaagtctc tggctottga cattgtggat gaggatatga 120
agctgatgat gtccacactg cccaagtctc tatccttgcc gacaactgcc cttcaaact 180
cttcagcct caccctgtca ggtatcaaag aagacaacag cttgctcaac cagggttct 240
tgcaggcaa gcccgagaag gcagcagtgg ccagaagcc ccgaagc cac ttcacgacac 300
ctgcccctat gtccagtgcc tgggaagacg gtggcctgcg gggggaccag gggaccagct 360
tttcatggca ggagaaagcc cggcagcttc tggggccgct tgaagcccag ccacactttt 420
cgggac 426
```

&lt;210&gt; 310

&lt;211&gt; 2627

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2627)

<223> v-myb avian myeloblastosis viral oncogene  
homolog-like 2 (MYBL2) gene.

```

<400> 310
gctgacgcct tcgagcgcgg ccc ggggccc ggagcggccg gagcagcccg ggtcctgacc 60
ccggcccggc tcccgtccg ggctctgccg gcgggcgggc gagcgcggcg cggtcgggc 120
cggggggatg tctcggcgga cgcgtgcga ggatctggat gagctgcact accaggacac 180
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ggacgagcag ctgagggccc tggtaggca gtttgacag caggactgga agttcctggc 300
cagccacttc cctaaccgca ctgaccagca atgccagtac aggtggctga gagttttgaa 360
tccagacctt gtcaaggggc catggaccaa agaggaagac caaaaagtca tcgagctggt 420
taagaagtat ggcacaaaagc agtggacact gattgccaag cacc tgaagg gccggctggg 480
gaagcagtgc cgtgaacgct ggcacaaaca cctcaaccct gaggtgaaga agtcttgctg 540
cgccgaggag gaggaccgca tcatctgcga ggcccacaag gtgctgggc accgctgggc 600
cgagatcgcc aagatgttgc cagggaggac agacaatgct gtgaagaatc actggaactc 660
taccatcaaa aggaaggtgg ac acaggagg cttcttgagc gaggccaaag actgcaagcc 720
cccagtgtac ttgctgctgg agctcgagga caaggacggc ctccagagtg cccagcccac 780
ggaaggccag ggaagtcttc tgaccaactg gccctccgtc cctcctacca taaaggagga 840
ggaaaacagt gaggaggaac ttgcagcagc caccacatcg aaggaaacagg agcccatcg 900
tacagatctg gacgcagtgc gaacaccaga gcccttgag gaattcccga agcgtgagga 960
ccaggaaggc tccccaccga aaacgagcct gccttacaag tgggtggtgg aggcagctaa 1020
cctcctcctc ccgctgttgg gttctagcct ctctgaagc ctggacttga tcgagtcgga 1080
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ggctctgtcc cctgtcactg agaatagcac cagtctgtcc ttcttgatt cctgtaacag 1440
cctcacgccc aagagcacac ctgttaagac cctgcccttc tcgcctccc agtttctgaa 1500
cttctggaac aaacaggaca cattggagct ggagagcccc tcgctgacat ccac cccagt 1560
gtgcagccag aaggtggtgg tcaccacacc actgcaccgg gacaagacac ccctgcacca 1620
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catcagggac gacatcaggc ccgagaagca gaagaggaag cctgggctgc ggccgagccc 1860
catcaagaaa gtccggaagt ctctggtct tgacattgtg gatgaggatg tgaagctgat 1920
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gttccctccc caaggccaca gggagctccg tcagcttctc ccaagcccac gtcaggcctg 2520
gcctcatctc agacctgct taggatggg gatgtggcca ggggtgctcc tgtgtcacc 2580
ctctcttggt gcattttttt ggaagaataa aattgcctct ctctttg 2627

```

<210> 311

<211> 442

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(442)

<223> 3' terminal sequence. transforming growth  
factor, beta receptor iii (betaglyc an, 300kd)

(TGFB3) gene.

&lt;400&gt; 311

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cccagactca aggagtgtgt aaagggttaa tagccagata gtagaaccag tgaggagatg 60
cggccaaaga ttctttatat ctgaaccaag atgtaaaaca agaaatgctt tgaggctttc 120
taagcgatcc tcctgtctaa tttgcacctt tgtctggatg cacacttctg accttgctgc 180
cacaacctgt ggggttctga tgtgtccctt gatgggtgct gccctcaggg actgcacct 240
gacaagtgtt aaggcaacat tcctttcttg tgcccggggc caaaaccaat gctgatgacc 300
ttatcagctt cctgtttctt ccatacttg catacaccac tggcaaaatg tcttaatggc 360
aaattttcta tttcttacag ggnctacagg aaatttgaaa atgg accaaa ttcagggaac 420
cacaggtttt gtggccatt tc 442
```

&lt;210&gt; 312

&lt;211&gt; 315

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(315)

<223> 5' terminal sequence. transforming growth  
factor, beta receptor iii (betaglycan, 300kd)  
(TGFB3) gene.

&lt;400&gt; 312

```
taacaaggag gtatcactga gcttatttta gctgcaaagt ggcatcatat tattccattt 60
aatgaaattc acctcaagcc ctttttgaca tattaaatat atgggatata tttaa ggcaa 120
gagaagtaag gcaatccaaa tgagtgcctt tttccaatct cagcactgtc ttgngngaatt 180
tggtgacact attcagataa ccaactggag accgacagat ttgccatgca tttgcatctt 240
gctagagttt ggtttttatg aaagggccta ttttttttta agttgacata ttttgagtgg 300
gaaacactca cccta 315
```

&lt;210&gt; 313

&lt;211&gt; 4208

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(4208)

<223> transforming growth factor, beta receptor  
iii (betaglycan, 300kd) (TGFB3) gene.

&lt;400&gt; 313

```
tctttaagat ttgtagctac taagaagaa aggagctttt tttccttggg ctttcaaact 60
gaaagaaccg catgagcctg acggcgcatg gtcttaacat caggctgtgc aggaagaagc 120
tatctgcaga tggatgccag cacacacaag gaagcagagc tctggcaaca ttgagtcaaa 180
gcaaggacac aacatcagag ggacggcaga gaatccttgt gtgtagtctt tgggtggcagt 240
ttgaaaattg caaggaggga cttaagact acttctgatt tgcaaagatg gtctgtgctc 300
cgagcaggct aaagtgactg gacgagacgc actgttgagg aaataaaaaat gacttcccat 360
tatgtgattg ccacttttgc cctgatgagc ttctgtttag cca ctgcagg tccagagcct 420
ggtgacactg gtgaactgtc acctgtcagt gcctcccatc ctgtccaggc cttgatggag 480
agcttcactg ttttgtcagg ctgtgccagc agaggcacia ctgggctgcc acaggaggtg 540
```

203/292

```

catgtctctga atctcgcact ggcgcagggg cctggccagc tacagagaga ggtcacactt 600
cacctgaatc ccatctcctc a gtcacatc caccacaagt ctgtttgtgtt cctgctcaac 660
tccccacacc ccctggtgtg gcatctgaag acagagagac ttgccactgg ggtctccaga 720
ctgttttttg tgtctgaggg ttctgtggtc cagttttcat cagcaaaactt ctccttgaca 780
gcagaaacag aagaaaggaa cttcccccat ggaaatgaac atctgttaaa ttgggcccga 840
aaagagtatg gagcagttac ttcatcacc gaactcaaga tagcaagaaa catttatatt 900
aaagtggggg aagatcaagt gttccctcca aagtgaaca tagggaagaa ttttctctca 960
ctcaattacc ttgctgagta ccttcaaccc aaagcagcag aagggtgtgt gatgtccagc 1020
cagccccaga atgaggaagt acacatcatc gagctaata cccccaactc taacccttac 1080
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ttacttctc tgccttaaat atatcccata tatttaatat gtcaaaaagg gcttgagggtg 4140
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tccttgtt

4208

<210> 314  
<211> 468  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(468)  
<223> 3' terminal sequence. peroxiredoxin 2  
(PRDX2) gene.

<400> 314  
tnnttttttt tttncacott tccctaatac ttnatnggtn acctctaggc ctgtgtgcgg 60  
ctgggtgggc ttgggggagg gcgtcactat tcagcttcta ggtggaggca tgagaaggcc 120  
ttggctaggc cctccagggt cccatactgt ggagtttga gggcaggtc tggcctttcc 180  
tgggtcagca tagggcaccc aggtgggggn acaggtggac acccagcaca ggcacctagg 240  
caggggcaca agctcantat cnttagcca gcctaattgt ntttgg agaa atattccttg 300  
ctgtcatcca cgttgggttt aatcgtgtca ctgccaggtt tccagccagc gggacaaant 360  
ttcccatgt tcgtttgtgt attgggaagg cctgggacca gccgcagagt tnatccacg 420  
gagngtccca aaggnaaatc attaaacagt gattttggcn aaggaaaa 468

<210> 315  
<211> 394  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(394)  
<223> 5' terminal sequence. peroxiredoxin 2  
(PRDX2) gene.

<400> 315  
acttcaaggc cacagcgggtg gttgatggcg ccttcaaaga ggtga agctg tccgactaca 60  
aagggaagta cgtggctctc tttttotacc ctctggactt cacttttgtg tgccccaccg 120  
agatcatcgc gttcagcaac cgtgcagagg acttccgcaa gctgggctgt gaagtgtctg 180  
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ggaggcttgg gccccctgaa catc cccctg cttgctgacg tgaccagacg cttgtctgag 300  
gattacggcg tgctgaaaac agatgagggc attgctaaca ggggcctctt tatcatcgat 360  
gggcaagggt gttcctttcg ccagatcaat gtta 394

<210> 316  
<211> 937  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>

205/292

<221> misc\_feature  
<222> (1)..(937)  
<223> peroxiredoxin 2 (PRDX2) gene.

<400> 316  
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tctagccttt gccacgcag ctttcagtca tggcctccgg taacgcg cgc atcggaaagc 120  
cagcccctga cttcaaggcc acagcgtgg ttgatggcg cttcaaagag gtgaagctgt 180  
cggactacaa agggaaagtac gtggctcctt ttttctacc cttggacttc acttttgtgt 240  
gccccaccga gatcatcgcg ttcacaaccg tgaagaggac ttccgcaaag ctgggctgtg 300  
aagtgtcggg cgtctcgggt gactc tcagt tcacccacct ggcttggatc aacaccccc 360  
ggaaagaggg aggcttgggc ccttgaaca tccccctgct tgctgacgtg accagacgt 420  
tgtctgagga ttacggcgtg ctgaaaaacg atgaggcat tgcttacagg gccctcttta 480  
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taggtgcctg tgctgggtgt ccacctgtgc cccacctgg gtgcc ctatg ctgacctagg 780  
aaaggccaga cctgccctc caaatccac agtatggag cctggagggc tagcaaggcc 840  
ttctcatgcc tccacctaga agctgaatag tgacgcctc cccaagccc accagccgc 900  
acacaggcct agaggttaacc aataaagtat tagggcc 937

<210> 317  
<211> 451  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(451)  
<223> 5' terminal sequence. v-fos fbj murine  
osteosarcoma viral oncogene homolog (FOS) gene.

<400> 317  
gctagacaca tgagctgaag accgagccct ttgatgactt cctgttccca gcatcatcca 60  
ggcccagtgg ctctgagaca gcccgctccg tgccagacat ggacctatct gggtccttct 120  
atgcagcaga ctgggagcct ctgcacagtg gctcccctgg gatggggccc atggcacagn 180  
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gcaaggcagc agcagcaatg agccttcctc tgactcgttc agctnaccca cgggtcgtggc 360  
cctgtgaggg gccaggggaa ggggaggcag ncggcaacna caagttgcca ttgtccgagt 420  
tngttgattt anagagagga gaaacaaatt t 451

<210> 318  
<211> 2084  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(2084)  
<223> v-fos fbj murine osteosarcoma viral oncogene  
homolog (FOS) gene.

<400> 318  
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ctcggcccct cgcccggctt tgccaaaccg ccacgatgat gttctcgggc ttcaacgcag 180  
actacgagc gtcac cctc cgctgcagca gcgcgtcccc ggccggggat agcctctctt 240  
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cagaccaact agaagatgag aagtctgctt tgacagccga gattgccaa ctgctgaagg 720  
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<210> 319

<211> 240

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(240)

<223> 3' terminal sequence. retinoblastoma -binding  
protein 7 (RBBP7) gene.

<400> 319

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gggaacagca agcacttagt ttgagaaaat gaggacttaa aacagttgan tcaaaggcaa 120  
taccctgcta cttgtattta aaatcaatgg tgatgttatt tcttangca cattctctc 180  
ttccctaata gctacaatnt gatacagtac gcaacagctc acttgaaagt gctagantca 240

<210> 320

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<211> 457  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(457)  
<223> 5' terminal sequence. retinoblastoma -binding  
protein 7 (RBBP7) gene.

<400> 320  
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ccgttcagtg gcttctctgaa gtgactaaac ctgaaggaaa agattatgcc cttcattggc 180  
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gtggcctttg ttctgtaaca ggnaaaattg aatgtgaaat taaaatcaat tcacgaagga 360  
gaagttaaac cgtgctcgtt aacatggccg cagantcctt cacatccatt gcttacaaan 420  
acaccctctt gcttgatggt gttggnnttt tgactat 457

<210> 321  
<211> 1946  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(1946)  
<223> retinoblastoma -binding protein 7 (RBBP7)  
gene.

<400> 321  
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ggagagagag agaagagcgc ctcagacctc ggtacccgcg agcggggagg aggcaggaaa 120  
gaaggacgcg gcgtctgggg agcaccagg cagcaagacg gggcccgggc tttcgacagt 180  
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ccgttcagtg gcttctctgaa gtgactaaac ctgaaggaaa agatt atgcc cttcattggc 480  
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aagtaaaccg tgctcgttac atg ccgcaga atcctcacat cattgctaca aaaacaccat 720  
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agcagggtat tgcctttgat tcaactgttt taagtcctca ttttctcaaa ctaagtgtt 1860
gctgttccca aatatgcaag aataactttt acactttttc cttccaacac ttcttgattg 1920
gctttgcaga aataaagttt taaaat 1946

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&lt;210&gt; 322

&lt;211&gt; 365

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(365)

<223> 3' terminal sequence. kiaa1075 protein  
(KIAA1075) gene.

&lt;400&gt; 322

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gggcc 365

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&lt;210&gt; 323

&lt;211&gt; 400

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(400)

<223> 5' terminal sequence. kiaa1075 protein  
(KIAA1075) gene.

&lt;400&gt; 323

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agaccccaga ggctccagt cccaccaaca tgagcacagc gncagacctc ctgcgtcagg 180
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cttnttttc gccgccatta tccagtggaa cagcatcacc 400

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<210> 324  
<211> 489  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(489)  
<223> 5' terminal sequence. atp-binding cassette,  
sub-family c (cftr/mrp), member 5 (ABCC5) gene.

<400> 324  
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cgacccctc agtgcccttag atgcccatgt ggaanccaca tncctcaata gtgctatccg 240  
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gagggaantg atggatttta aatggtgatt atggttacct ttttaattaa cntgtgttg 420  
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ttcacagtt 489

<210> 325  
<211> 5838  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(5838)  
<223> atp-binding cassette, sub-family c  
(cftr/mrp), member 5 (ABCC5) gene.

<400> 325  
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cagctcttgc taatcagtgt ctacactgg cgtagaagtt tttgtactgt aaagagacct 5580
acctcagggt gctggttgc t g t g t g t t g t g t g t t c c c g c a a a c c c c c t t t g t g c t g t 5640
ggggtgggta gctcagggtg gcgtgggtcac tgctgtcatc agttgaatgg tcagcgttgc 5700
atgtcgtgac caactagaca ttctgtcgcc ttagcatgtt tgctgaacac cttgtggaag 5760
caaaaatctg aaaatgtgaa taaaattatt ttggattttg taaaaaaaaa aaaaaaaaaa 5820
aaaaaaaaa aaaaaaaaaa 5838

```

&lt;210&gt; 326

&lt;211&gt; 385

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(385)

<223> 3' terminal sequence. cadherin 1, type 1,  
e-cadherin (epithelial) (CDH1) gene.

&lt;400&gt; 326

```

aanganatat taacaaaatt gtttaataaa atttataaaa atgcatcttt gagaatactt 60
tntcagctt gaattgtttt ccttttccac ccccaaagaa aatacacaat tatcagcacc 120
cacacatgta tacactcaaa actacagtga catt ctctac acagnnctat attcgatata 180
gottgaactg ccgaaaaatc angacaattc caaaagggtga ttgcagggtt gatttttttc 240
tccaaaacac ttgaganaca gtaaagctat ttcaacaaag gtcttttncct tgattgtcaa 300
aggttgaaat tcacatttna ntannagggg ntccnaatca ngntoctcac taccacctac 360
ccctcancta accccctttg gggcc 385

```

&lt;210&gt; 327

&lt;211&gt; 423

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(423)

<223> 5' terminal sequence. cadherin 1, type 1,  
e-cadherin (epithelial) (CDH1) gene.

&lt;400&gt; 327

```

ggcacgagca aganaggagt tctctgatgc agaaattatt gggctctttt agggtaagaa 60
gtttgtgtct ttgtctggcc acatcttgac taggtattgt ctactctgaa gacctttaat 120
ggcttccctc tttcatctcc tgagtatgta acttgcaatg ggcagctatc c agtgacttg 180

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ttctgagtaa gtgtgttcat taatgtttat ttagctctga agcaagagt atatactcca 240
gggacttaga atagtgccta aagtgtctga gccaaagaca gagcggaact atgaaaagt 300
ggcttgagaga tggcaggaga gcttgcatt gagcctgggc aatttnagca aactgatgtc 360
tgaggatgat tcgaggtggg tcttacctca tctactgnaa aattctggta aggaatggga 420
ggg 423

```

&lt;210&gt; 328

&lt;211&gt; 4828

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(4828)

<223> cadherin 1, type 1, e-cadherin (epithelial)  
(CDH1) gene.

&lt;400&gt; 328

```

agtggcgctg gaactgcaaa gcacctgtga gcttgcgga gtcagttcag actccagccc 60
gctccagccc ggcccgaacc gaccgcaacc ggcgcctgcc ctgcctcggc gtcccggcc 120
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cacgggtccc cgccgccacc tggagagagg ccgcgtcctg ggcagagtga attttgaaga 300
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agatggtgtg attacagtca aaaggcctct acggtttcat aaccacaga tccatttctt 420
ggtctacgcc tgggactcca cctacagaaa gttttccacc aaagtcacgc tgaatacagt 480
ggggcaccac caccgcccc cgcccatca ggctccgtt tctggaatcc aagcagaatt 540
gtccacattt cccaactcct ctctggcct cagaagacag aagagagact gggttattcc 600
tcccacagc tgcccagaaa atgaaaaagg cccatttctt aaaaacctgg ttcagatcaa 660
atccaacaaa gacaaagaag gcaaggcttt ctacagcatc actggccaag gagctgacac 720
acccctgtt ggtgtcttta ttattgaaag agaaacagga tgggtgaagg tgacagagcc 780
tctgtagata gaacgcattg ccacatacac tctcttctct cacgctgtgt catccaacgg 840
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gcccgaattc acccaggagg tctttaaggg gtctgtcatg gaaggtgctc ttccaggaa 960
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taacaggaac acaggagtca tcagtgtggt caccactggg ctggaccgag agagtctccc 1140
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cacgtacaca gccctaata tagctacaga caatggttct ccagttgcta ctggaacagg 1860
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gcctgtcgaa gcaggattgc aaattcctgc cattctggg attcttgag gaattcttgc 2280
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```

gcccttactg cccccagagg atgacacccg ggacaacggt tattactatg atgaagaagg 2400
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attttggtta accataaaaa aaaaaaaa 4828

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&lt;210&gt; 329

&lt;211&gt; 471

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(471)

<223> 5' terminal sequence. zinc finger protein  
144 (mel-18) (ZNF144) gene.

&lt;400&gt; 329

```

attcggcaca tgattccact tccgtttccc agggcaacgc tcccagtc cccacccc cc 60
gaccccgga tcatgcatcg gactacacgg atcaaaatca cagagctgaa cccacacctc 120

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atgtgtgccc tctgcgggg gtacttcac gacgccacca ctatcgtgga gtgcctgcat 180  
tccttctgca aaacctgcat cgtgcgtac ctggagacca acaatactg ccccatgtgt 240  
gacgtgcagg tccataaaac ccggccgctg ctgagca ttc aggtctgaca aaacatttca 300  
agacattgtc ttacaaattg gtccctgggg ctttttaaag atggagattg aaacgggagg 360  
cgggatttct tatggcaggc gttaccctt ggacgggagg tcccccaac ggnttccaat 420  
tgagggaccg ngggcgaggg ttttnggga ggcagggaga aggggggttt t 471

&lt;210&gt; 330

&lt;211&gt; 2227

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2227)

<223> zinc finger protein 144 (mel -18) (ZNF144)  
gene.

&lt;400&gt; 330

gagagcccga acaggaagag ggtacagctt tgtg caggtc acatgcccac tgcagccctc 60  
cagcctctgg tccccagagc ggactttgga agctgaactg cttttgttgc tggaagactt 120  
atgttataat ttaccttggg tggaccaggg tcgtacaaaa gggcaacgct cccagctccc 180  
cccactcccg accccggaat catgcatcgg actacacgga tcaaaatcac agagctgaac 240  
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ggggatgggg acaaaagagaa aacaggggtg cgc ttcctgc gatgccagc agccatgacc 720  
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gcatcacctc ctctctttgc agtggaact ttgtgcaaag aatagatagt tctgcctctt 1920  
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tcacctgggg cctagagtgg aagtgggggt ggggttaacct cacacaagca cagatcccag 2160  
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acactcg 2227

<210> 331  
<211> 254  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(254)  
<223> 3' terminal sequence. macrophage stimulating  
1 (hepatocyte growth factor -like) (MST1) gene.

<400> 331  
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gacacgcgtg aagacagctg gccagcggga ccttgccgat actcgggttg ggattataat 180  
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cacaggcccc caca 254

<210> 332  
<211> 362  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(362)  
<223> 5' terminal sequence. macrophage stimulating  
1 (hepatocyte growth factor -like) (MST1) gene.

<400> 332  
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acgtctgcgt gatgaccagc cgccatcaat cctggacccc ccagaccagg tgcagtttga 120  
gaagtgtggc aagagggttg atcggctgga tcagcggcgt tccaagctgc gctgggtggg 180  
ggccatccgg gcaactcacc ctggacagtc agcttgcgga atcggcaggg ccagcatttc 240  
tgcggngngt ctctagttaa ggagcagtn gatactgactn cccggaagtg cttctcctcc 300  
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ag 362

<210> 333  
<211> 2219  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(2219)  
<223> macrophage stimulating 1 (hepatocyte growth  
factor-like) (MST1) gene.



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&lt;400&gt; 333

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gctacatgcg gtggtgcccg ggccttggca ggaggatgtg gcagatgctg aagagtgtgc 180
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gtaccggggc accatggcca cgaccgtggg tggcctgccc tgccaggctt ggagccacaa 420
gttcccgaat gatcacaagt acacgcccac tctccggaat ggcttgaag agaacttctg 480
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gatcgagcga gagtctctgt acctccccg ctgcgggtcc gaggcacagc cccgccaaga 840
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&lt;210&gt; 334

&lt;211&gt; 431

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(431)

<223> 3' terminal sequence. glutathione  
s-transferase pi (GSTP1) gene.

&lt;400&gt; 334

```
gaaaggaagg caaactctgc cnccc gctca gagtcccccc aaccctcact gtttcccgtt 60
gccattgatg gggagggtca cgtactcagg ggaggccagg naggcntgna gcttggggccg 120
ggcactgagg cgcacacat atgtgagag cagggggaac gcatccagc agccagggt 180
agggaccnca tggatcagca gcaagtccag caggttntag tcagcgaagg agntctggtc 240
tcccacaatg aaggtcttgc ctccctggtt ctgggacagc aggttctcaa aaggcttcag 300
```

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ttgccccgggc agtgccttca catagtcatc cttgcccccc tcatagtgtg tntagatgag 360  
ggagatgtat ttgcagcgga ggtcctccac gccgttcatt tcacctgtcc accagggctg 420  
nctcctttt t 431

<210> 335  
<211> 305  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(305)  
<223> 5' terminal sequence. glutathione  
s-transferase pi (GSTP1) gene.

<400> 335  
nattcgccac aggtcgccac catgccgccc tacaccgtgg totatttccc agttcgaggc 60  
cgctgcctgt cggcaatgct gctggcagat cagggccaga gctggaagga ggaggtngtg 120  
accgtggaga cgtggcagga gggctcactc aaagcctcct gcctatacgg gcagctcccc 180  
aagttccagg acggagacct naccctgtac cagt ccaata ccacctgcg tcacctgggc 240  
cgcacccttg ggctnctatg ggaaggacca gcaggangca gccctggtgg acatngtgaa 300  
tgacg 305

<210> 336  
<211> 737  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(737)  
<223> glutathione s-transferase pi (GSTP1) gene.

<400> 336  
ggagtttcgc cgccgcagtc ttgccacca tgccgccta caccgtggtc tatttcccag 60  
ttcgaggccg ctgcgcggcc ctgcgcatgc tgctggcaga tcagg gccag agctggaagg 120  
aggaggtggt gaccgtggag acgtggcagg agggctcact caaagcctcc tgcctatac 180  
ggcagctccc caagttccag gacggagacc tcaccctgta ccagtccaat accatcctgc 240  
gtcacctggg ccgcaccctt gggctctatg ggaaggacca gcaggaggca gccctggtgg 300  
acatggtgaa tgacggcgtg gag gacctcc gctgcaaata catctccctc atctacacca 360  
actatgaggc gggcaaggat gactatgtga aggcactgcc cgggcaactg aagccttttg 420  
agaccctgct gtcccagaac cagggaggca agaccttcat tgtgggagac cagatctcct 480  
tcgctgacta caacctgctg gacttgctgc tgatccatga ggtcctagcc cctggctgcc 540  
tggtatgcgtt cccctgctc tcagcatatg tggggcgccct cagcgcccg cccaagctca 600  
aggccttccct ggctccctcct gactacgtga acctcccat caatggcaac gggaaacagt 660  
gagggttggt gggactctga gcgggaggca gagtttgccct tcctttctcc aggaccaata 720  
aaatttctaa gagagct 737

<210> 337  
<211> 372  
<212> DNA  
<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(372)

<223> 3' terminal sequence. b-cell cll/lymphoma 2  
(BCL2) gene.

&lt;400&gt; 337

```
gtgggnctgt gttgaaacag gccacgtaaa gcaactctct aaaggtcaaa ccaccataga 60
tttgaatctg ctggtcattc gccatctgga tttttaactg aatgaatctc atgggtttaa 120
ccaaacatgc atgtaatcct gaataccatg anttaaatgc gganttgccc agggacgagg 180
aaaccttcaa gaaacaaggt caaagggaca ncagatata a ctgtcacant aaacanttct 240
gttgacgtgg gaaatgcaca tgacttggtt gaaacaaagc tcctcagtgg gccagtga 300
tccnggggtt ttcttagggt aggctgagga ctcaggggct tatctcacct tctcaggaat 360
gctttttgaa gg                                     372
```

&lt;210&gt; 338

&lt;211&gt; 508

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(508)

<223> 5' terminal sequence. b-cell cll/lymphoma 2  
(BCL2) gene.

&lt;400&gt; 338

```
nttcggcaca gacttttttt aagctaccaa ttg tgccgag aaaagcattt tagcaattta 60
tacaatatca tccagtacct taaacctga ttgtgtatat tcatatattt tggatacgca 120
ccccccaact cccaatactg gctctgtctg agtaagaaac agaatcctct ggaacttgag 180
gaagtgaaca ttccggtgac ttccgcatca ggaaggctag agttaccagc agcatcaggc 240
cgccacaagt gctgtctttt aggagaccga agtcgcgaga acctgcctgt gtcccagctt 300
ggaggcctgg gtcctgggaa ctgagccggg gccctcactg gccttccttc caggggatgg 360
atcaacaggg gcagtgtggt cttccgaatg tctgggaagc tgatgggagc tcagantttc 420
cactgtcaag aaagaggcag ttaggagggg tttgggtggg gcttgttcac ctgg ggggcc 480
ttccaggtag ggcctttttt aagtggga                                     508
```

&lt;210&gt; 339

&lt;211&gt; 445

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(445)

<223> 3' terminal sequence. proliferating cell  
nuclear antigen (PCNA) gene.

&lt;400&gt; 339

219/292

```

tttttttant caaaagtttg aaattcaagt aactttatit aaattcaaaa acaattctta 60
aaactgcatt tagagtcaag acccttttgt attataaaaa tcacaagtat ttctaagaga 120
caaaaatact tctagggttaa ctagaccaga tctgactt tg gactttattc tttaaacaan 180
ttgcagagan tagagaaaaa antaggttat ttacagaaaa caatatctac atatgtactt 240
ngnggtacaa ntttggtga cagaaaagac ttcaggata tgctgggcàt cttaggaagn 300
cagttctcaa agggnccttag gttttatttn cttggatttt taaggattgc cctaagganc 360
ccttcttcat cctcgnctctt gggggngggc aggtaggtnt tttaggtgtc ccctatccc 420
ganttttata ctctncaccg gggggg 445

```

&lt;210&gt; 340

&lt;211&gt; 437

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(437)

<223> 5' terminal sequence. proliferating cell  
nuclear antigen (PCNA) gene.

&lt;400&gt; 340

```

gctccagcgt tgtaaacctg cagagatgga ctgctccac gtctctttgg tgcagctcac 60
cctgcggtct gagggcttcg acacctaccg ctgcgaccgc aacctggcca tggggtgaac 120
ctcaccagta tgtccaaaat actaaaatgc gccggcaatg aagatatcat tacactaagg 180
gccgaagata acgcggatac cttggcgcta gtatttgaag caccaaacca ggagaaagt 240
tcagactatg aaatgaagtt gatggattta gatgttgaac aacttngaag tccagaacag 300
gagtacagct gtgtagtaaa gatgccntct ggtgaatttg c acgtatatg ccgagatctc 360
agccatattg ggagatgctg ttgtaatttc ctgtgncaaa agacgggagt gaaaattttt 420
ctgcaagtgg gagnact 437

```

&lt;210&gt; 341

&lt;211&gt; 1231

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1231)

<223> proliferating cell nuclear antigen (PCNA)  
gene.

&lt;400&gt; 341

```

aggctcagc cggtcgtcgc gacgttcgcc cgctcgctct gaggtccttg aagccgaaac 60
tagctagact ttctctcttc ccgctgcct gtacggcgtg tgttgccact ccgccaccat 120
gttcgaggcg cgcctggtcc agggctccat cctcaagaag gtgttgagg cactcaagga 180
cctcatcaac gaggcctgct gggatattag tccagcgggt gtaaacctgc agagcatgga 240
ctcgtccac gtctctttgg tgcagctcac cctgcggtct gagggcttcg acacctaccg 300
ctgcgaccgc aacctggc ca tgggcgtgaa cctcaccagt atgtccaaa tactaaaatg 360
cgccggcaat gaagatatca ttactaag ggccgaagat aacgcggata ccttggcgct 420
agtatttgaa gcaccaaacc aggagaaagt ttcagactat gaaatgaagt tgatggattt 480
agatgttgaa caacttgga ttccagaaca ggagtacagc tgtgtagtaa agatgccttc 540
tggtgaattt gcacgtatat gccgagatct cagccatatt ggagatgctg ttgtaatttc 600
ctgtgcaaaa gacggagtga aattttctgc aagtggagaa cttggaaatg gaaacattaa 660

```

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```
attgtcacag acaagtaatg tcgataaaga ggaggaagct gttaccatag agatgaatga 720
accagttcaa ctaacttttg cactgaggta cctgaact tc tttacaaaag ccactccact 780
ctcttcaacg gtgacactca gtatgtctgc agatgtaccc cttgttgtag agtataaaat 840
tgcggatatg ggacacttaa aatactactt ggctcccaag atcgaggatg aagaaggatc 900
ttaggcattc ttaaaattca agaaaataaa actaagctct ttgagaactg cttctaagat 960
gccagcatat actgaa gtct tttctgtcac caaatttgta cctctaagta catatgtaga 1020
tattgttttc tgtaaataac ctattttttt tctctattct ctccaatttg tttaaagaat 1080
aaagtocaaa gtctgatctg gtctagttaa octagaagta tttttgtctc ttagaaatac 1140
ttgtgatttt tataatacaa aagggtcttg actctaaatg cagttttaag aagtg ttttt 1200
gaatttaaat aaagttactt gaatttcaaa c 1231
```

&lt;210&gt; 342

&lt;211&gt; 383

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(383)

<223> 3' terminal sequence. adenovirus 5 ela  
binding protein (BS69) gene.

&lt;400&gt; 342

```
ttttttttt aaacacacan gttttcacgc tgtagtaact tggaaatgtg caaccogtgt 60
caacagagac agaaaagcca aagtaacacg aatctcactt tcatgcagct atcagttaaa 120
tattacatac tctggaatga ttttacacca aaaatattt c cacaattact tgctctcata 180
ggggtggatc gaagtcttaa aacttgaaaa acaatcaaag aaggttaagt gttctcgggt 240
ctgacatctc catcagcgcc acacactgtg gngaacactg gactaattac acagcaacaa 300
ggaggggaac gatgatgcc agttactgca taatttaggg tacattgtat ggaatggggg 360
gctactgggg gtactttttt tac 383
```

&lt;210&gt; 343

&lt;211&gt; 483

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(483)

<223> 5' terminal sequence. adenovirus 5 ela  
binding protein (BS69) gene.

&lt;400&gt; 343

```
gttnaaattg cagggactgg ggtaatcttt tactgagctg gatcttagag aaaatgaata 60
tttaaatttt aaagtttgca catttcactt ttgtcctaac atgagtgtt gtaacaaaat 120
aaacaacaaa aacaaagcca aaaactacct ttatccatat gtgaaattat agatgaggca 180
tacgaatttg tttaatgctt ccttccctt cccacatata atctcactgc ctattatctg 240
gtgtcacctc atgtatcgta agttaatact aaaagaagag aaagcactta agtttcacag 300
aagccgttat gttttagagt aatgggggtca ttgcctaagt gaactccatc actgtacaca 360
gaatgaagga nttaatgcc tgttaatttt cttgttattt aagg atgccg tggatttggt 420
aaaaggctct gtattttgct gggatgtctg gggtaggga ggccttacct ataggggntg 480
ggg 483
```

<210> 344  
<211> 2722  
<212> DNA/RNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(2722)  
<223> adenovirus 5 ela binding protein (BS69)  
gene.

<400> 344  
ggagcataat gctaaaagaag taaacaggtc atggcacggt taacaaaaag acgacaggcg 60  
atacaaaagc tatccagcat ctttgggcag ccattgagat tata cggaac cagaagcaga 120  
ttgccaacat tgaccgtatt acaaaatgtg aaacaactac attattcttg aacctatggt 180  
gattttttaca tcattacaca gatattgtcat ttccattagt tgtatcattg ttataaactg 240  
gtatatgtct cgagtccacg gtatgcaccc taaagagacc acccgtcagc tgagcttagc 300  
tgtgaaagat ggtcttattg tc gaaactct aacagtgggc tgcaaagggt caaaagctgg 360  
tattgaacaa gaaggatatt ggttgccagg agatgagatt gactgggaaa cagaaaatca 420  
tgactgggtat tgttttgaat gccatttgcc tggagagggt ttgatattgt acctgtgttt 480  
tcgtgtgtat cattccaagt gtttgtctga tgagttcagg cttagagaca gcagtagtcc 540  
ctggcagtgcc ccagtttgca ggagcattaa gaagaagaat acaaacaaac aggagatggg 600  
cacatacctc agatttcattg tctcccgcat gaaggagagg gctatagatc ttaataaaaa 660  
ggggaaggac aataaacacc cgatgtacag gaggctggtg cactcagctg tggacgttcc 720  
caccattcaa gagaagtga atgaaggga ataccgaagt ta tgaagagt tcaaagctga 780  
tgccaattg cttctccaca ataccgtgat tttctatgga gcagacagtg agcaagctga 840  
cattgcgagg atgctatata aagacacatg tcatgagctg gatgaactgc agctttgcaa 900  
gaattgcttt tacttgtcaa atgctcgtcc tgacaactgg ttctgttatc cttgtatacc 960  
taatcatgag ctggtttggg ctaaaatgaa aggttttggg ttttggccag ccaaagtcac 1020  
gcagaaagaa gacaatcaag tcgacgttcg cttctttggc caccaccacc agagggcctg 1080  
gattccttct gaaaacattc aagatatcac agtcaacatt catcggtctg acgtgaagcg 1140  
cagtatgggt tggaaaagg cctgtgatga gctggagctg catcagcgtt tcctacgaga 1200  
aggagatatt tggaaatcta agaattgagga ccgagggtgag gaagaggcag aatccagtat 1260  
ctctccacc agtaatgagc agctaaaggc cactcaagaa ccaagagcaa agaaaggacg 1320  
acgtaataca agtgtggagc ccaaaaagga agaaccagag cctgaaacag aagcagtaag 1380  
ttctagccag gaaataacca cgatgcctca gccc atcgaa aaagtctccg tgtcaactca 1440  
gacaaagaag ttaagtgcct cttcaccaag aatgctgcat cggagcagcc agaccacaaa 1500  
cgacggcgtg tgtcagagca tgtgccatga caaatacacc aagatcttca atgacttcaa 1560  
agaccggatg aagtcggacc acaagcggga gacagagcgt gttgtccgag aagctctgga 1620  
gaagctgctg tctgaaatgg aagaagaaaa gagacaagct gtaaataaag ctgtagccaa 1680  
catgcagggt gagatggaca gaaaatgtaa gcaagtaaag gaaaagtgtg aggaggaatt 1740  
tgtagaagaa atcaagaagc tggcaacaca gcacaagcaa ctgatttctc agaccaagaa 1800  
gaagcagtggt tgctacaact gtgaggagga ggccatgtac cactgctg ct ggaacacatc 1860  
ctactgctcc atcaagtgcc agcaggagca ctggcacgcg gagcacaagc gcacctgccg 1920  
ccgaaaaga tgaagctggc ctttcccgga gtcaccccgga tgattactct tttcagacac 1980  
agcgggtttt gtttccaaga agccaaaatt gtttagaatt tgcttcccat tttgcaccag 2040  
cctttaaaca cttttcgtga ag aaattttg cacagtagtt taaatctttt gttaatgctc 2100  
ctccgaagtt tttcaggggg taaaagttaac atcagtggag ggtattatct taaataaatt 2160  
ttaattgaga atttgttgca ttttcagcaa attttaaaac atttttaggt tttacagaga 2220  
ttttaacctt taaacaacag atctttaaaa aaccagtgaa tacaagtgtg tttacaaaag 2 280  
aaacatttag aatagatctg aatgtaagaa ctacagaact gtttcagaaa taaaacatac 2340  
taccttgatg tgacattttt ttcttaacct tgttgagctg gttttgttca gcttaattta 2400  
ctgttcaaag gcattatctg ttggtcacac cagtgggtat atgattgaat ttagggaaca 2460  
gggttgacac agcagggtca gtccgtcata tttttt ctta aatatttccc aattgtgttt 2520  
ttcattatct cttttcaata tataactttt ataacaaatt attagctttg atctttagt 2580  
ttaaaattgc agggaactgg ggtaatcttt tactgagctg gatcttagag aaaatgaata 2640  
tttaaatctt aaagtttgcc acatttcatc tttgtcctaa catgagtgtc tgtaacaaaa 2700

222/292

taaaacaaca aaaacaaagc ct

2722

<210> 345  
<211> 363  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(363)  
<223> 3' terminal sequence. matrix  
          metalloproteinase 11 (stromelysin 3) (MMP11) gene.

<400> 345  
gcatgcagca tectgagtgg tagcgtcgat ctgagagggc acccctctcc agtcagtggc 60  
cctgcgggna cggngactgt ctacacgccg ggtgctgggg tggaaacgcc agtagtccct 120  
gcctcggaag aagtagatct tggtcttctc gggaccccag accaaggc ag catggaccgg 180  
gaacctcacc agggcccagc tcggtgaggg gtgcggggcc cagggaactg cttttcaccg 240  
tcgtacaccc agtacttgag caccttgga agaaccaaat gtgggcccgg cttaccacagc 300  
attggccttt tcgccacagg gctggggcag tccctgccag tngcgagaag ccaattttg 360  
gca 363

<210> 346  
<211> 2260  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(2260)  
<223> matrix metalloproteinase 11 (stromelysin 3)  
          (MMP11) gene.

<400> 346  
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cgccctcctg cccccgatgc tgctgctgct gctccagccg ccgcccgtgc tggcccgggc 120  
tctgccgccc gacgtccacc acctccatgc cgagaggagg gggccacagc cctggcatgc 180  
agccctgccc agtagcccgg cacctgcccc tgccacgcag gaagcccccc ggccctgccag 240  
cagcctcagg cctccccgct gtggcgtgcc cgacccatct gatgggctga gtgcccgcaa 300  
ccgacagaag aggttcgtgc tttctggcgg gcgctgggag aagacggacc tcacctacag 360  
gacccctcgg ttcccatggc agttggtgca ggagcagggt cggcagacga tggcaga ggc 420  
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tgacatcatg atcgacttcg ccagggtactg gcatggggac gacctgccgt ttgatgggcc 540  
tgggggcatc ctggcccatg ccttcttccc caagactcac cgagaagggg atgtccactt 600  
cgactatgat gagacctgga ctatcgggga tgacc agggc acagacctgc tgcaggttggc 660  
agcccataga tttggccacg tgctggggct gcagcacaca acagcagcca aggccttgat 720  
gtccgccttc tacaccttcc gctaccact gagctcagc ccagatgact gcaggggcgt 780  
tcaacaccta tatggccagc cctggcccac tgtcacctcc aggaccccag ccctggggccc 840  
ccaggctggg atagacacca atgagattgc accgctggag ccagacgccc cgccagatgc 900  
ctgtgaggcc tcctttgacg cggctctccac catccgaggc gagctctttt tcttcaaagc 960  
gggctttgtg tggcgccctc gtgggggcca gctgcagccc ggctaccacg cattggcctc 1020  
tcgccactgg cagggaactgc ccagccctgt ggacgctgcc ttcgaggatg ccca gggcca 1080  
catttggttc ttccaagggtg ctgagtactg ggtgtacgac ggtgaaaagc cagtcctggg 1140

223/292

```

ccccgcaccc ctcaccgagc tgggcctggt gaggttcccg gtccatgctg ccttggtctg 1200
gggtcccag aagaacaaga tctacttctt ccgaggcagg gactactggc gtttccaccc 1260
cagcaccggg cgtgtagaca gtcccgtgc c ccgaggggc actgactgga gaggggtgcc 1320
ctctgagatc gacgctgcct tccaggatgc tgatggctat gcctacttcc tgcgcggccg 1380
cctctactgg aagtttgacc ctgtgaaggt gaaggctctg gaaggcttcc ccgctctcgt 1440
gggtcctgac ttctttgggt gtgccgagcc tgccaacact ttctctgac catggcttgg 1500
atgccctcag ggggtgctgac cctgcccagg ccacgaatat caggctagag acccatggcc 1560
atctttgtgg ctgtgggcac caggcatggg actgagccca tgtctcctgc agggggatgg 1620
ggtgggggtac aaccaccatg acaactgccg ggagggccac gcaggctcgtg gtcacctgcc 1680
agcgactgtc tcagactggg caggagggtt ttggcatgac tt aagaggaa gggcagtctt 1740
gggaccogct atgcaggctc tggcaaacct ggctgccctg tctcatccct gtccctcagg 1800
gtagcaccat ggcaggactg ggggaactgg agtgtccttg ctgtatccct gttgtgaggt 1860
tccttccagg ggctggcact gaagcaaggg tgctggggcc ccatggcctt cagccctggc 1920
tgagcaactg ggctgtaggg caggggcact tcctgaggtc aggtcttggg aggtgcctgc 1980
atctgtctgc cttctggctg acaatcctgg aaatctgttc tccagaatcc aggccaaaaa 2040
gttcacagtc aaatggggag ggggtattct catgcaggag accccaggcc ctggaggctg 2100
caacatacct caatcctgtc ccaggccgga tcctcctgaa gcccttttcg cagcac tgct 2160
atcctcaaaa gccattgtaa atgtgtgtac agtgtgtata aaccttcttc ttcttttttt 2220
tttttaaact gaggattgtc attaaacaca gttgttttct 2260

```

&lt;210&gt; 347

&lt;211&gt; 273

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(273)

<223> 3' terminal sequence. hypothetical protein  
mgc13071 (MGC13071) gene.

&lt;400&gt; 347

```

atgtttattg aacgtaacag tatatttcat gtagtttccc ataatttttt catgtactaa 60
ctcatgtaat tctttgtttt ttagagatct gaagtgat tt tacctttact tccttcactt 120
taagccaatc atgaaatttc agtgatttct ggggtgaggg cgaaagggtg tgttacgaat 180
catcggggct gtggccagnt tgctcacgg aggtgcagg aggtggggc ctcactaggg 240
canctggagg agcacggact gccctgccgg cag 273

```

&lt;210&gt; 348

&lt;211&gt; 330

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(330)

<223> 5' terminal sequence. hypothetical protein  
mgc13071 (MGC13071) gene.

&lt;400&gt; 348

```

ggagtacaga acattgtggt aggggaaggg actcactttc tcatcccatg tgtacaaaaa 60
ccaattatct ttgactgctg ttctcaacca cgtagtcgnc cagtcacac tggtagcaaa 120
gatttacaga atgtcaacat cacactgtgc atcctcttcc ggcccatcac tagccagctt 180

```



224/292

```

cctcgcatct tcaccagcat tggagaggac tacgatgagt gtgtgctgcc gttcattacc 240
acggagatcc tcaagtcact ggtggctcgc tttgatgctg gagaactaat caccagaggg 300
gagcttggtt tccagccngg tgaagnacca                               330

```

&lt;210&gt; 349

&lt;211&gt; 1168

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:prime r

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1168)

<223> hypothetical protein mgc13071 (MGC13071)  
gene.

&lt;400&gt; 349

```

aaatgatgat agtagtacct acagtatagt gctgttagaa ttacatgagt tagatgtgga 60
ggtcagagtg gaagcaggtg tgagagggtc ccgcagaaga aaacatggct gccaaagtgt 120
ttgagtccat cggcaagttt ggccctggcct tagctgttgc aggaggcatg gtgacctctg 180
ccttatgtaa tgtggatgct gggcacagag ctgccatctt tgaccaattc cgtggagtac 240
agaacattgt ggtaggggaa gggactcact ttctcatccc atgtgtacaa aaaccaatta 300
tctttgactg ctgtttctca ccacgtagtg cgccagtcac c actggtagc aaagatttac 360
agaatgtcaa catcacactg tgcacacctt tccggcccat cactagccag ctccctcgca 420
tcttcaccag cattggagag gactacgatg agtgtgtgct gccgttcatt accacggaga 480
tctcaagtc actggtggct cgctttgatg ctggagaact aatcaccag agggagctgg 540
tctccagcca ggtgagcaac aaccttatgg agtgagcagc cacctttggg ctctattctg 600
acgacgtgtc ttgacacat ctgaccttct tgaaggagtt aacagacagg tggcccccca 660
ggaagcagag agcgccagat ttgtggtgga aaaggcggcc atcatctctg ctgaggggtg 720
ctccaaggca gctgagctga tcgccaaetc actggccact gcaggggacg gccagagcga 780
gctgtgcaag ctggaagctg cagaagacat tgcataccag ctctcatgct ctcggaacat 840
cacctgcctg ccggcagggc agtccgtgct cctccagctg ccctagttag gccccagcct 900
acctgcacct ccgtgaggca actggggcac agccccgatg attcgttaaca ccacctttcg 960
ccctaccccc agaaatcact gaaatttcat gattggctta aagtgaagga agtaaaggta 1020
aaatcacttc agatctctaa aaaacaaaga attacatgag ttagtacatg aaaaaattat 1080
gggaaactac atgaaatata ctgttacgtt caataaacat tagcttctgt atataaaaaa 1140
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa                               1168

```

&lt;210&gt; 350

&lt;211&gt; 315

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(315)

<223> 5' terminal sequence. interleukin enhancer  
binding factor 2, 45kd (ILF2) gene.

&lt;400&gt; 350

```

ctggctttga aatcagttct ncgtgatgct acagtgaaga ttctcattac aacagtgcc 60
cccaatcttc gaaaactgga tccagaactc catttgata tcaaagtatt gcagagtgcc 120
ttagcagcca tccgacatgc ccgctggtc gaggaataat cttctcagtc cacagttaaa 180
gttcnccanc agantactga aggacttgag gattcgtttt cnggctttg agc cctcaca 240

```

225/292

ccnnggatnc ttgaactact aggn cattat gctgtgatga acaacccac caganagcct 300  
 ttgcnctaa acgtt 315

<210> 351  
 <211> 1552  
 <212> DNA/RNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(1552)  
 <223> interleukin enhancer binding factor 2, 45kd  
 (ILF2) gene.

<400> 351  
 cggttggtgc ggcttcatt gttcgtgttt taaggcgcca tgaggggtga cagaggccgt 60  
 ggtcgtggtg ggcgcttttg ttccagagga ggcccaggag gag ggttcag gccctttgta 120  
 ccacatatcc catttgactt ctatttgtgt gaaatggcct ttccccgggt caagccagca 180  
 cctgatgaaa ctctccttcag tgaggccttg ctgaagagga atcaggacct ggctcccaat 240  
 tctgctgaac aggcattctat cctttctctg gtgacaaaa taaacaatgt gattgataat 300  
 ctgattgtgg ctccagggac a ttgaagtg caaattgaag aagttcgaca ggtgggatcc 360  
 tataaaaagg ggacaatgac tacaggacac aatgtggctg acctgggtgt gatactcaag 420  
 attctgccaa cggttgaagc tgttgctgcc ctggggaaca aagtcgtgga aagcctaaga 480  
 gcacaggatc cttctgaagt tttaaccatg ctgaccaacg aaactggctt tgaaatcagt 540  
 tcttctgatg ctacagtga gattctcatt acaacagtgc cacccaatct tcgaaaactg 600  
 gatccagaac tccattttga tatcaaagta ttgcagagtg ccttagcagc catccgacat 660  
 gcccgctggt tcgaggaaaa tgcttctcag tccacagtta aagttctcat cagactactg 720  
 aaggacttga ggattcgttt tcttggtctt gagccccca c acctggat ccttgacctg 780  
 ctaggccatt atgctgtgat gaacaacccc accagacagc ctttggccct aaacgttgca 840  
 tacaggcgct gcttcagat tctggctgca ggactgttcc tgccaggttc agtgggtatc 900  
 actgaccctt gtgagagtgg caactttaga gtacacacag tcatgacctt agaacagcag 960  
 gacatggtct gctatacagc tcagactctc gtccgaatcc tctcacatgg tggctttagg 1020  
 aagatccttg gccaggaggg tgatgccagc tatcttgcct ctgaaatctc tacctgggat 1080  
 ggagtgatag taacaccttc agaaaaggct tatgagaagc caccagagaa gaaggaagga 1140  
 aggaagaag aggagaatac agaaaagaac acctcaagga gaggaagaag aaagcatgg a 1200  
 aactcaggag tgacattccc ttactcctt ttctaccca agggaaagac tggagcctaa 1260  
 gctgcctgct actggcttta catggtgaca gacattccgt ggataggaag atagcaggag 1320  
 aaagtaactc catagagtgt cattccactg gttgatattg gcttagctgc cagtctccca 1380  
 tttgtgacct atgccatcca tctataatgg agg ataccaa catttcttcc taatattcta 1440  
 taatctccaa ctctgaaaa cccctctctc aactaatact ttgctgttga aatgttgtga 1500  
 aatgttaagt gtctggaaat tttttttct aagaaaaact attaaagtac tt 1552

<210> 352  
 <211> 396  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<220>  
 <221> misc\_feature  
 <222> (1)..(396)  
 <223> 3' terminal sequence. hypothetical protein  
 flj11307 (FLJ11307) gene.

226/292

&lt;400&gt; 352

ctccattaca ggggtttttgc cacttgctgt gaggataggg ccctgagttc ttacctctaa 60  
ggtactggag gtttc agttg tagaatttcc agtattattg cttgagtttg aagacactgt 120  
ttcattttta ctttcattat ctgatttttc atcggaactc atacattcaa tatctgcatc 180  
aaagcctggt ggatatccca ttgctgcaa taccttcacc gctacgtgaa agttttgctg 240  
ttttcttgga tggctctgag gcttcatatg ttgtgccatc cacatctaca gacattg tga 300  
agactggggg catgaacggg ggccagactg aagataagaa gctatactga agcacaggcc 360  
tgatctgaat taagcntcat tagtggcatt ccataa 396

&lt;210&gt; 353

&lt;211&gt; 1858

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1858)

<223> hypothetical protein flj11307 (FLJ11307)  
gene.

&lt;400&gt; 353

tcgatgaaag atcctccgga cttattggac aggcagaaat gccgaacgc cttggcgtct 60  
cttcgacatg ccaaattggt tcaggcaagg gcaaattgat taaaatcatg tgtaat tgtc 120  
ctccgcattc tgcgtgattt gtgcaacaga gtcccacat gggcaccatt gaaaggatgg 180  
ccactagaac ttatatgtga aaagtctata ggtacttgta atagacctt gggcgctggg 240  
gaggccttga gacgagtaat ggagtgttg gcatctggaa tactacttcc tgggggtcct 300  
ggtcttcatg atccttgtga gcgagacca acag atgtc tgagctatat gaccatccag 360  
caaaaagaag atattaccca cagtgcacag catgcactca gactatcagc ctttggccag 420  
atttacaaag tgctggagat ggacccctt ccatctagta agccttttca gaagtattcc 480  
tggtcagtta ctgataaaga aggtgctggg tcttcagctc taaagaggcc atttgaagat 540  
ggattagggg atgataaaga cccaacaag aagatgaaac gaaacttaag gaaaattctg 600  
gatagtaaag caatagacct tatgaatgca ctaatgaggc taaatcagat caggcctggg 660  
cttcagtata agctcctatc tcagtctggc ccggttcatg cccagctctt cacaatgtct 720  
gtagatgtgg atggcacaac atatgaagcc tcaggaccat ccaagaaaac agca aaactt 780  
cacgtagcgg tgaaggattt gcaggcaatg ggatatccaa caggctttga tgcagatatt 840  
gaatgtatga gttccgatga aaaaatcagat aatgaaagta aaaaatgaaac agtgtcttca 900  
aactcaagca ataatactgg aaattctaca actgaaacct ccagtacctt agaggtaaga 960  
actcagggcc ctatcctcac agcaagtggc aa aaacctg taatggagct caatgaaaaa 1020  
agaagaggtc tcaagtatga actcatctca gagactggtg gaagccatga caagcgcttt 1080  
gtaatggagg tagaagtaga tggacagaaa ttcagaggcg cagggtccaa taagaaagt 1140  
gcaaaggcga gtgcagcttt agctgccttg gagaaactgt tttctggacc caatgcggca 1200  
aataataaga aaaagaagat tatccctcag gcaaaggcg ttgtgaatac agctgtgtct 1260  
gcagcagtc aagctgttcg gggcagagga agagggaactc taacaagggg agcttttgtt 1320  
ggggcgacag ctgctcctgg ctacatagct ccaggctatg gaacaccata tggttacagc 1380  
acagctgccc ctgcctatgg ttaccccaag agaattggtc tgttac ccgt tatgaaattt 1440  
ccaacatata ctgttcccca ctactcattc ttttagcaaa tgacagaagc taattcctat 1500  
tgaacaacaa tacagtacaa cacagaatgt tagagaaaaa gcctttttat cctgctttct 1560  
ttgaacacat acttgatcaa aattatttgt aaagaacatc tttcctactt tttgatttta 1620  
acaaatgcaa atttagttct ctaaaacttg aaaaaaaaaa aagaaaccag ttctgtgaaa 1680  
acggtacctc atttctggaa aataacttat accagccctt ctgttctagg gaaataaaaag 1740  
tctagcagtt caaagtttaa gttttaagag acgtatcaga ttatgtaaaa ttaaatttgt 1800  
gaaggatgta tagagtctca aacactgatc acaataaac tgctttgtg taacacag 1858

&lt;210&gt; 354

&lt;211&gt; 242

&lt;212&gt; DNA

227/292

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(242)

<223> 5' terminal sequence. v -myb avian  
myeloblastosis viral oncogene homolog (MYB) gen e.

&lt;400&gt; 354

```
agaaccccag cstatcaaaag gtcaatctta gaaagctctc caagaactcc tacaccattc 60
aaacatgcac ttgcagctca agaaattaaa tacgggtccc tgaagatgct acctcagaca 120
ccctctcatc tagtagaaga tctgcaggat gtgatcaaac aggaatctga tgaatctgga 180
attgttgctg agtttcaacg aaaatggacc acccttactg aacgaaaatc ntacaacgag 240
gt                                         242
```

&lt;210&gt; 355

&lt;211&gt; 3225

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(3225)

<223> v-myb avian myeloblastosis viral oncogene  
homolog (MYB) gene.

&lt;400&gt; 355

```
ggcggcagcg ccctgccgac gccggggagg gacgcaggca ggcggcgggc agcgggaggc 60
ggcaccocgg tgctccccgc ggctctcggc ggagccccgc cgcccgccgc gccatggccc 120
gaagaccccg gcacagcata tatagcagtg acgaggatga tgaggacttt gagatgtgtg 180
accatgacta tgatgggctg cttcccaagt ctggaaagcg tcacttgggg aaaacaaggt 240
ggaccgggga agaggatgaa aaactgaaga agctggtgga acagaatgga acagatgact 300
ggaaaagtta tgccaattat ctcccgaatc gaacagatgt gcagtgccag caccgat ggc 360
agaaagtact aaaccttgag ctcatcaagg gtccttggac caaagaagaa gatcagagag 420
tgatagagct tgtacagaaa tacggtccga aacgttggtc tgttattgcc aagcacttaa 480
aggggagaat tggaaaacaa tgtagggaga ggtggcataa ccacttgaat ccagaagtta 540
agaaaacctc ctggacagaa gaggaagaca gaatt attta ccaggcacac aagagactgg 600
ggaacagatg ggcagaaatc gcaaagctac tgccctggacg aactgataat gctatcaaga 660
accactggaa ttctacaatg cgtcgggaagg tcgaacagga aggttatctg caggagtctt 720
caaaagccag ccagccagca gtggccacaa gcttcagaa gaacagtcac ttgatggggt 780
ttgctcaggc tccgcctaca gctcaactcc ctgccactgg ccagcccact gtaacaacg 840
actattccta ttaccacatt tctgaagcac aaaatgtctc cagtcattgt ccataccctg 900
tagcgttaca tgtaaatata gtcaatgtcc ctcagccagc tgccgcagcc attcagagac 960
actataatga tgaagaccct gagaaggaaa agcgaataaa ggaattagaa ttgct cctaa 1020
tgtcaaccga gaatgagcta aaaggacagc aggtgctacc aacacagAAC cacacatgca 1080
gctaccocgg gtggcacagc accaccattg ccgaccacac cagacctcat ggagacagt 1140
cacctgtttc ctgtttggga gaacaccact ccactccatc tctgccagcg gatcctgggt 1200
ccctacctga agaaagcgcc tcgccagcaa ggtgcatgat cgtccaccag ggcaccattc 1260
tgataatgt taagaacctc ttagaatttg cagaaacact ccaatttata gattctttct 1320
taaacacttc cagtaaccat gaaaactcag acttggaat gccttcttta acttccaccc 1380
ccctcattgg tcacaaattg actgttacaa caccatttca tagagaccag actgtgaaa 1440
ctcaaaagga aaatactgtt tttagaacc cagctatcaa aaggatcaat ttagaaagct 1500
ctccaagaac tcctacacca ttcaaactg cacttgcagc tcaagaaatt aaatacgggt 1560
ccctgaagat gctacctcag acaccctctc atctagtaga agatctgcag gatgtgatca 1620
```

228/292

```

aacaggaatc tgatgaatct ggatttgttg ctgagtttca aga aaatgga ccacccttac 1680
tgaagaaaat caaacaagag gtggaatctc caactgataa atcaggaaac ttcttctgct 1740
cacaccactg ggaaggggac agtctgaata cccaactgtt cacgcagacc tcgcctgtgc 1800
gagatgcacc gaatattctt acaagctccg ttttaatggc accagcatca gaagatgaag 1860
acaatgttct caaagcat tt acagtaccta aaaacaggtc cctggcgagc cccttgacgc 1920
cttgtagcag tacctgggaa cctgcatcct gtggaagat ggaggagcag atgacatctt 1980
ccagtcaagc tcgtaaatac gtgaatgcat tctcagcccg gacgctggtc atgtgagaca 2040
tttccagaaa agcattatgg ttttcagaac agttcaagtt gacttgggat atatcat tcc 2100
tcaacatgaa acttttcatg aatgggagaa gaacctatct ttgttgttgt acaacagttg 2160
agagcacgac caagtgcatt tagttgaatg aagtcttctt ggatttcacc caactaaaag 2220
gatttttaaa aataaataac agtcttacct aaattattag gtaatgaatt gtagccagtt 2280
gttaatatct taatgcagat ttttttaaaa aaaaacataa aatgatttat ctggtatttt 2340
aaagatcca acagatcagt attttttctt gtgatgggtt ttttgaaatt tgacacatta 2400
aaagtgactc cagtatttca cttttctcga tcactaaaca tatgcatata tttttaaaaa 2460
tcagtaaaag cattactcta agtgtagact taataccatg tgacatttaa tccagattgt 2520
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agttttctgt tagcttgctt taaaaattat tactgtaaga aatagtttta taaaaaatta 2640
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attttttatt gtggtttttt tgttattgtt ggtttataca agcatgcgtt gcacttcttt 2940
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ataattggg agttctgat ttgatccgca tcccctgtgg tttctaagt tatggtctca 3060
gaactgttgc atggatcctg tgtttgcaac tggggagaca gaaactgtgg ttgatagcca 3120
gtcactgcct taagaacatt tgatgcaaga tggccagcac tgaacttttg agatatgac g 3180
gtgtacttac tgccttgtag caaaataaag atgtgccctt atttt 3225

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&lt;210&gt; 356

&lt;211&gt; 369

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(369)

<223> 3' terminal sequence. zinc finger protein 9  
(a cellular retroviral nucleic acid binding  
protein) (ZNF9) gene.

&lt;400&gt; 356

```

gtagttaa at gcagaaagtc ggtttttttc caccctttc ctccttttac acggcaagta 60
aagctcactg gcctgggagtg tgctctatc tgccaacctt tggccagtga agaggattca 1 20
gagaaaataa tacaaccatc aatcagaaaa aggaggggag acaaaggaaa ataattaggc 180
tgtagctcaa ttgtgcattc ccgtgcaagg tgccctgact cgccacagcg gtaacagttg 240
acttcacttg tcttgcgtga gttgatggct acatgaccag tttcaccaca cctatagcac 300
ttcacttttg tgcagtcttt tttgaatgtg tcccgaattc tcccacaaga atancctttc 360
tgctcanct 369

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&lt;210&gt; 357

&lt;211&gt; 1500

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(1500)  
<223> zinc finger protein 9 (a cellular retroviral  
nucleic acid binding protein) (ZNF9) gene.

<400> 357  
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ccgctgcggg cccgctccga cgcggaagat ctgactgcag ccatgagcag caatgagtgc 120  
ttcaagtgtg gacgatctgg ccaactggggc cgggaatgtc ctactggtgg aggccgtggg 180  
cgtggaatga gaagccgtgg cagaggtggg ttacctcgg atagagggtt ccagtttggt 240  
tcctcgtctc ttccagatat ttgttatcgc tgtggtgagt ctggcatct tgccaaggat 300  
tgtgatcttc aggaggatgc ctgctataac tgcggtagag gtg gccacat tgccaaggac 360  
tgcaaggagc ccaagagaga gcgagagcaa tgctgtaca actgtggcaa accaggccat 420  
ctggctcgtg actgcgacca tgcagatgag cagaaatgct attcttggg agaattcggg 480  
cacattcaaa aagactgcac caaagtgaag tgctatagg gtggtgaaac tggcatgta 540  
gccatcaact gcagcaagac aagtgaagtc aactgttacc gctgtggcga gtcagggcac 600  
cttgacggg aatgcacaat tgaggctaca gcctaattat tttcctttgt cgcctcctcct 660  
ttttctgatt gatggttgta ttattttctc tgaatcctct tcactggcca aaggttggca 720  
gatagaggca actcccaggc cagtgcgctt tacttgccgt gtaaaaggag gaaaggggtg 780  
gaaaaaaacc gactttctgc atttaactac aaaaaaagt tatgtttagt ttggtaggag 840  
tgttatgtat aatgctttgt taaagaacct ctttccgtg ccactggtga atagggattg 900  
atgaatggga agagttgagt cagaccagta agcccgtcct gggttccttg aacatgttcc 960  
catgtaggag gtaaaaccaa ttctggaagt gtctatgaac t tccataaat aactttaatt 1020  
ttagtataat gatggtcttg gattgtctga cctcagtagc tattaataa catcaagtaa 1080  
tatctgtatc aggccctaca tagaacatac agttgagtgg gagtaacaa aaagataaac 1140  
atgcgtgtta atggctgttc gagagaaatc ggaataaaaag cctaaacagg aacaacttca 1200  
tcacagtgtt gatgtt ggac acatagatgg tgatggcaaa ggtttagaac acattatatt 1260  
caaagactaa atctaaaacc cagagtaaac atcaatgctc agagttagca taatttggag 1320  
ctattcagga attgcagaga aatgcatttt cacagaaatc aagatgttat tttgtatatac 1380  
tatatcactt agacaactgt gtttcatttg ctgtaatcag tttttaaaag tcaga tggaa 1440  
agagcaactg aagtctaga aaatagaaat gtaattttaa actattccaa taaagctgga 1500

<210> 358  
<211> 425  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(425)  
<223> 3' terminal sequence. camp responsive  
element modulator (CREM) gene.

<400> 358  
ttttttactt ctgcaagatc ttttatatta cacagtagag ttaaaaactg tagtaaatgt 60  
tcagatatatt aaatgagcac caaacactac aaagtgaac caacatggtt ctattaaaaa 120  
ctcncctttga ctatggcatt caaggacagc aatacaat ct tttttttttt taacaaagca 180  
actaatataa aaatctgcaa atgccatata ttcatatcta ggctattctt cncatatagg 240  
catgtcatta gatagacttt ctttctatct tttcngagg natTTTTTTT nggtttacnt 300  
ttattgnact gctggatgca ttatttttga tcatcctttc ctaaaatgnt ttaaagacct 360  
gcaataaatt ttattg cata ggacacnatt ggtgncacat agaattgggag cngcaagtat 420  
gtggc 425

<210> 359

230/292

<211> 232  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(232)  
<223> 5' terminal sequence. camp responsive  
element modulator (CREM) gene.

<400> 359  
ggatttagag ttaactagct caccactgcc tctgcctcca agctgccttt tagactgaat 60  
agcttttctt gttagcccta ctttaacatt tcttttgaag tgggtgtctg cttgaagagg 120  
gaaacacgtc atgaaactgt aatgcatgaa cagaactcag gagttgtctg gccagcttag 180  
tgctgccact ggtgacatgc caacttacca gatccgagct cctantgnng ct 232

<210> 360  
<211> 1431  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:prime r

<220>  
<221> misc\_feature  
<222> (1)..(1431)  
<223> camp responsive element modulator (CREM)  
gene.

<400> 360  
atgaccatgg aaacagttga atcccagcat gatggaagta taacagcttc tttgacagag 60  
agcaagtctg ctcatgtgca gactcagact gggcaaattt caatccctgc tttagctcag 120  
tgcagtgaagc tgagatcagg caccagaaga ggctcccag ctgtaactct agtgcagtta 180  
ccttcggggc aaactataca tgtccaggga gtaattcaga caccacagcc atgggttatt 240  
cagtcacag aaatacacac cgttcaggta gcagcaattg cagagacaga tgaatctgca 300  
gaatcagaag gtgtaattga ttctcataaa cgtagagaaa t cctttcacg aagaccctct 360  
tataggaaaa tactgaatga actgtcctct gatgtgcctg gtgttcccaa gattgaagaa 420  
gagagatcag aggaagaagg aacaccacct agtattgcta ccatggcagt accaactagc 480  
atatacaga ctagcacggg gcaatacatt gctatagccc aagggtggaac aatccagatt 540  
tctaaccag gatctgatgg tgttcaggga ctgcaggcat taacaatgac aaattcagga 600  
gctcctccac caggtgctac aattgtacag tacgcagcac aatcagctga tggcacacag 660  
cagttctttg tcccaggcag ccaggttgtt gttcaagctg ccactggtga catgccaaact 720  
taccagatcc gagctcttac tgctgctttg ccacaggag tggatgatgc tgcacgccc 780  
ggaagtgtgc acagtcccca gcagctggca gaagaagcaa cacgcaaacy agagctgagg 840  
ctaataaaaa acagagaagc tgcccgggag tgcgcagga agaagaaaga atatgtcaaa 900  
tgtcttgaaa atcgtgtggc tgtgcttgaa aaccaaaca agactctcat tgaggaaactc 960  
aaggccctca aagatcttta ttgccataaa gtagagtaac tgtctttgac ttggaccttg 1020  
tttactctaa tcaaggcagg agatgcagca gtccacttta ttgccatgtg gacttgtggg 1080  
aaggacacgt gtgaccctta agaatccagt ttggattagt gtttgaaatt gaattgggaa 1140  
tggtgttcca ggatgtgaa tgacagctga tcacacttac cgagcttact ttgatctggt 1200  
tgtcaatagc atgcaaaaaa tgctttgttt gccctttgct tctgcttttt tcagggaag 1260  
ctgccaaaga atgtcgacgt cgaaagaaag aatatgtaaa atgcctggag agccgagttg 1320  
cagtgtgga agtcagaac aagaagctta tagaggaact tgaaacctg aaagacattt 1380  
gttctcccaa aactgattac tagaaatatt taactatgaa ctgattacag a 1431

231/292

<210> 361  
<211> 457  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(457)  
<223> 3' terminal sequence. cathepsin b (CTSB)  
gene.

<400> 361  
caagttggag aaacctttta ttggcacagg cattccttgt taacttgaca ggtgaagct 60  
gtaatttttc aaaaacagta aaagctgggt tctcctaaac tattttcctt gtggtagtag 120  
agatcagtg gtcagaaaca actcctgacc acttggtttc cttttgagcc gcgtcattag 180  
gaggcaatct gtaaaactag cacaggctct ccgctgttcc actgggtcac ccacatg att 240  
agcagagtgc acgaaaaaat aaaacttcta ttaaagaatc atgctgagca caacatcaga 300  
gagggttgta cattgcaaac tcgatagatg cagggggcct gggagactgg cgttctccaa 360  
agggtccca acaccatctc tcctctgatt tctgtgacaa atgtggaagc tacttgcttg 420  
gagggtactgg gggaactgat gggggaactt tcatac cg 457

<210> 362  
<211> 401  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(401)  
<223> 3' terminal sequence. melan -a (MLANA) gene.

<400> 362  
atcatgcatt gcaacattta ttgatggagt tttcccaatt taatatttct catcatttcc 60  
tcacatgatt agtactgcta gcggacctac taaaatttta acactgactt attattagag 120  
atggcttgca tttttcctac accattccaa aggagaacat tagatgtctg tattaaattc 180  
aagcaaaagt gtgagagaaa taatttcagc atgtctcagg tgtctcgt g gcncttaagg 240  
tgaataaggt ggtggtgact gttctgcaga gagtttctca taagcagggt gagcattggg 300  
aaccacaggt tcacagtttt tctcttgaag agacactttg ctgtcccgat gatcaaacc 360  
ttcttgtggg catcttcctg ttaaggcaca ttgaggccaa c 401

<210> 363  
<211> 370  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(370)  
<223> 5' terminal sequence. melan -a (MLANA) gene.



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&lt;400&gt; 363

attaaggaag gtgtcctgtg ccttgaccct acaagatgcc aagagaagat gctcacttca 6 0  
 tctatggtta cccaagaag gggcacggcc actcttacac cacggctgaa gaggccgctg 120  
 ggatcggcat cctgacagtg atcctgggag tcttactgct catcggtgtg tggatttgta 180  
 gaagacgaaa tggatacaga gccttgatgg ataaaagtct tcatgttggc actcaatgtg 240  
 cttacaaga agatgcccac aagaagggtt tgatcatcgg gacagcaaag tgtctcttca 300  
 agagaaaaac tgtgaacctg tggttcccaa tgctccacct gcttatggag aaactctctg 360  
 cagaacagtc 370

&lt;210&gt; 364

&lt;211&gt; 1524

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1524)

&lt;223&gt; melan-a (MLANA) gene.

&lt;400&gt; 364

agcagacaga ggactctcat taaggaaggt gtctgtgcc ctgaccctac aagatgccaa 60  
 gagaagatgc tcacttcato tatggttacc ccaagaaggg gcacggccac tcttacacca 120  
 cggctgaaga ggccgctggg atcggcatcc tgacagtgat cctgggagtc ttactgctca 180  
 tcggctgttg gtattgtaga agacgaaatg gatacagagc cttgatggat aaaagtcttc 240  
 atgttggcac tcaatgtgcc ttaacaagaa gatgccaca agaagggttt gatcatcggg 300  
 acagcaaagt gtctcttcaa gagaaaaact gtgaacctgt ggttccc aat gctccacctg 360  
 cttatgagaa actctctgca gaacagtcac caccacctta ttcaccttaa gagccagcga 420  
 gacacctgag acatgtcgaa attatttctc tcacactttt gcttgaattt aatacagaca 480  
 tctaattgtc tcctttggaa tgggttagga aaaatgcaag ccactctctaa taataagtca 540  
 gtgttaaaat tttagtaggt ccgct agcag tactaatcat gtgaggaaat gatgagaaat 600  
 attaaattgg gaaaactcca tcaataaatg ttgcaatgca tgatactatc tgtgccagag 660  
 gtaatgttag taaatccatg gtgttatttt ctgagagaca gaattcaagt gggattctcg 720  
 gggccatcca atttctcttt acttgaaatt tggctaataa caaactagtc aggttttcga 780  
 accttgaccg acatgaactg tacacagaat tgttccagta ctatggagtg ctcacaaagg 840  
 atacttttac aggttaagac aaagggttga ctggcctatt tatctgatca agaacatgtc 900  
 agcaatgtct ctttgtgctc taaaattcta ttatactaca ataatatatt gtaaagatcc 960  
 tatagctctt tttttttgag atggagtttc gcttttgttg ccag gctgg agtgcaatgg 1020  
 cggatcttg gctcaccata acctccgctt cccagggtta agcaattctc ctgccttagc 1080  
 ctctgagta gctgggatta caggcgtgag ccactatgcc tgactaattt tgtagtttta 1140  
 gtagagacgg ggtttctcca tgttggtcag gctgggtctc aactcctgac ctcaggtgat 1200  
 ctgcccgcct cagcctccca aagtgtgga attacaggcg tgagccacca cgctggctg 1260  
 gatcctatat cttaggttaag acatataacg cagtctaatt acatttcact tcaaggctca 1320  
 atgtattctt aactaatgac aagtattttc tactaaacca gaaattggta gaaggattta 1380  
 aataagtaaa agctactatg tactgcctta gtgctgatgc ctgtgtactg ccttaaatg t 1440  
 acctatggca atttagctct cttgggttcc caaatccctc tcacaagaat gtgcagaaga 1500  
 aatcataaag gatcagagat tctg 1524

&lt;210&gt; 365

&lt;211&gt; 556

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:p rimer

&lt;220&gt;

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<221> misc\_feature  
<222> (1)..(556)  
<223> 3' terminal sequence. apr -1 protein (APR-1)  
gene.

<400> 365  
actattcggt aggccttttat tttctcttat gttctgcagt aactaaggaa aatcatggta 60  
aatgtcaatc ttcacacaac agcagacaca aagggtttca gaaacgtcag atatgaag aa 120  
atcctccatc cttcttcaac attttactgg gtatttcaac ttcaaaagaa cagcttattt 180  
ctataagtgc tgtacaagat catagattat gatggaacga cttcatttta gaacgtagc 240  
aaaactgtta tactaaatgt caatgacagg aaacaaagaa aaaaatttgt tcaattatat 300  
ttttaaacat attgttattc tcaacaaacg gaattt taaa acgaatacaa ttttcatta 360  
tcaaaaagca aacactctat ttgcgagttg aacaatgac actgacaca aatataaat 420  
acagtgtccc ccgcccccaa tcgacatcat tttccactta gggaccctgg catccactcc 480  
ctgggggtac ccgtgactcc ncctttacac cccccagggg ctggcctcag atctacctaa 540  
gggnggggat aacc cc 556

<210> 366  
<211> 464  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(464)  
<223> 5' terminal sequence. apr -1 protein (APR-1)  
gene.

<400> 366  
aacagcgcca aggaagctct ggtctggaaa gtgctgggga agttaggaat gcagcctgga 60  
cgtcagcaca gcatctttgg agatccgaag aagatcgta cagaagagtt tgtgcgcaga 120  
gggtacctga ttataaacc ggtgcccggt agcagtcggg tggagtatga gttcttctgg 180  
gggccccgag cacacg tga atcgagcaaa ctgaaagtca tgcattttgt ggcaagggtt 240  
cgtaaccgat gctctaaaga ctggccttgt aattatgact gggattcggg cgatgatgca 300  
gaggttgagg ctatcctcaa ttcaggtgct aggggttatt ccgcccctta agtagatctg 360  
gaggcagacc cttgggggtt gtaaaagaga gtnacaggta ccccaaaagg agtagatg nc 420  
aaggggccct aagttgcaaa atgatgtoga ttttggggcc gggg 464

<210> 367  
<211> 1476  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(1476)  
<223> apr-1 protein (APR-1) gene.

<400> 367  
ctggaagaat tcgcgtggca ggagaggcgg ggccaatttt gctgagcttt ctgcggggct 60  
tgcagctgcg gcaagtgtcg gcggcggctg ctgcgcgaag tcagctggcg tgggaactac 120  
cctttgtagc tgagaacggc ttgtttattg ctacaaagac totattgaca ttggtagctt 180  
cagcggcagc agcttct tac ggtataaagc tggtgcttcc tgaagaggct acaagcatcc 240

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```
ttccctagga ctgctgtaag ctttgagcct ctagcaggag acatgcctcg gggacgaaag 300
agtcggcgcc gccgtaatgc gagagccgca gaagagaacc gcaacaatcg caaaatccag 360
gcctcagagg cctccgagac ccctatggcc gcctctgtgg tagcgagcac ccccgaga c 420
gacctgagcg gccccgagga agacccgagc actccagagg aggcctctac caccctgaa 480
gaagcctcga gcaactgcca agcacaaaag ctttcagtgc cccggagcaa ttttcagggc 540
accaagaaaa gtctcctgat gtctatatta gcgctcatct tcacatggg caacagcgcc 600
aaggaagctc tggcttgga agtgctgggg aagttag gaa tgcagcctgg acgtcagcac 660
agcatctttg gagatccgaa gaagatcgtc acagaagagt ttgtgcgcag agggtagctg 720
atttataaac cgggtgcccc tagcagtcgg gtggagtatg agttcttctg ggggccccga 780
gcacacgtgg aatcgagcaa actgaaagtc atgcattttg tggcaagggt tcgtaaccga 840
tgctctaaag actgg ccttg taattatgac tgggattcgg acgatgatgc agaggttgag 900
gctatcctca attcaggtgc taggggttat tccgccccct aagtagatct gaggcagacc 960
cttgggggtg taaaagagag tcacaggtag cccaaggagt agatgccagg gtcctaagtt 1020
gaaaatgatg tcgattgggg gcgggggaca ctgtatttga tatttgtag cagtga tcac 1080
tggtcaactg cgaaatagag tgtttgcttt tgataatgga aaattgtatt cgttttaaaa 1140
ttcgtttgtg tgagaataac aatatgttta aaaatataat tgaacaaatt tttttctttg 1200
tttctgtca ttgacattta gtataacagt tttgctaacg ttctaaaatg aagtcgttcc 1260
atcataatct atgatcttgt acagcactta tagaaataag ctgttctttt gaagttgaaa 1320
taccagtaa aatgttgaag aaggatggag gatttcttca tatctgacgt ttctgaaacc 1380
ctttgtgtct gctgttgtgt gaagattgac atttaccatg attttcctta gttacttgac 1440
gtcttgtatc tctttttatt ttcggattgc ttatca 1476
```

&lt;210&gt; 368

&lt;211&gt; 436

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(436)

<223> 3' terminal sequence. ets variant gene 5  
(ets-related molecule) (ETV5) gene.

&lt;400&gt; 368

```
cgtttttttg ctttaaatat caaaactaca aaaatcagtt tataaactgt ttttccaaaa 60
caaccaccaa aacaaaacaa tcccccaaat cagggcacaa caaataactg tcaaaagtgt 120
taatcgccct tctcctaaaa taaaagtcac ccacactcag ccacgtgatt gggaagagaa 180
agggggcttg ctctacttgg cgaccacatg gccgggtggt tcccaa gagt agccatggtt 240
tatgattttg agaaccacgg agngcgaaac agctgttctg actgcccccc tttttctaga 300
caagggttaa ttttcagat tcagctagaa gagctttoca atgtttaaga tgtattttta 360
acccttaatg gtttgagcct cccaactta gcctacttac ttttcnaagg gtttgtgatt 420
tttcaacaaa ttgtgc 436
```

&lt;210&gt; 369

&lt;211&gt; 414

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(414)

<223> 5' terminal sequence. ets variant gene 5  
(ets-related molecule) (ETV5) gene.

&lt;400&gt; 369

```
ggttgctcgg cgctggggca tccagaagaa ccggccagcc atgaactatg acaagctgag 60
ccgctctctc cgctattact atgaaaaggg catcatgcag aagggtggctg gagagcgata 120
cgtctacaaa ttgtctctgtg acccagatgc cctcttctcc atggctttcc cggataacca 180
gcgtccggtc ctgaaggcag agtccgagtg ccacctcagc gaggaggaca ccctgccgct 240
gacccacttt gaagacagcc ccgcttacct cctggacatg gaccgctgca gcagcctccc 300
ctatgccgaa gggttgctta ctaagtttct gagtggcgga gtgnccaaac ctagggagct 360
agcagttccc attcagggca aacaagnggc agtgnggtt gtt ttgtgtt tttt 414
```

&lt;210&gt; 370

&lt;211&gt; 249

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(249)

<223> 5' terminal sequence. cd69 antigen (p60,  
early t-cell activation antigen) (CD69) gene.

&lt;400&gt; 370

```
ataataagga aacgtgttca cttattgact attatagaat ggaactcatg gaaatctgtg 60
tcagtggatg ctgctctgtg gtccgaagtc ttccatagag actttgtgaa aaaaaatttt 120
atagtgtctt gggaattttc ttccaaacag aactatggaa aaaaaggaag aaattccagg 180
aaaatctgca ctgtgggctt ttattgccat gagctagaag catcacaggg tgaccaataa 240
cccngacgc 249
```

&lt;210&gt; 371

&lt;211&gt; 1702

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1702)

<223> cd69 antigen (p60, early t-cell activation  
antigen) (CD69) gene.

&lt;400&gt; 371

```
agactcaaca agagctccag caaagacttt cactgtagct tgacttgacc tgagattaac 60
tagggaatct tgagaataaa gatgagctct gaaaattggt tcgtagcaga gaacagct ct 120
ttgcatccgg agagtggaca agaaaatgat gccaccagtc cccatttctc aacacgtcat 180
gaagggctct tccaagttcc tgtcctgtgt gctgtaatga atgtggtctt catcaccatt 240
ttaatcatag ctctcattgc cttatcagtg ggccaatata attgtccagg ccaatacaca 300
ttctcaatgc catcagacag ccatgtttct tcatgc tctg aggactgggt tggctaccag 360
aggaaatgct actttatttc tactgtgaag aggagctgga cttcagccca aaatgcttgt 420
tctgaacatg gtgctactct tgctgtcatt gattctgaaa aggacatgaa ctttctaaaa 480
cgatacgagc gtagagagga aactggggtt ggactgaaaa aggaacctgg tcacctatgg 540
aagtggtaaa atggcaaaga atttaacaac tgggtcaacg ttacaggggtc tgacaagtgt 600
gtttttctga aaaacacaga ggtcagcagc atggaatgtg agaagaattt atactggata 660
tgtaacaaac cttacaaata ataaggaaac atgttcactt attgactatt atagaatgga 720
actcaaggaa atctgtgtca gtggatgctg ctctgtggtc cgaagtcttc cataga gact 780
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```

ttgtgaaaaa aaattttata gtgtcttggg aattttcttc caaacagaac tatggaaaaa 840
aaggaagaaa ttccaggaaa atctgcactg tgggctttta ttgcatgag ctagaagcat 900
cacaggttga ccaataacca tgccaagaa tgagaagaat gactatgcaa cctttggatg 960
cactttatat tattttgaat ccagaaataa tgaa ataact aggcgtggac ttactattta 1020
ttgctgaatg actaccaaca gtgagagccc ttcatgcatt tgcactactg gaaggagtta 1080
gatgttggta ctagatactg aatgtaaaca aaggaattat ggctggtaac atagggtttt 1140
agtctaattg aatcccttaa actcaggag catttataaa tggacaaatg cttatgaaac 1200
taagatttgt aatatttctc tctttttaga gaaatttgcc aatttacttt gttatttttc 1260
cccaaaaaga atgggatgat cgtgtattta tttttttact tcctcagctg tagacaggtc 1320
cttttcgatg gtacatatat ctttgccttt ataacttttt atacagtgtc ttacagagaa 1380
aagacataag caaagactat gaggaatatt tgcaagacat agaatagt gt tggaaaatgt 1440
gcaatatgtg atgtggcaaa tctctattag gaaatattct gtaatcttca gacctagaat 1500
aatactagtc ttataatagg tttgtgactt tcctaaatca attctattac gtgcaatact 1560
tcaatacttc atttaaaata tttttatgtg caataaaatg tatttgtttg tattttgtgt 1620
tcagtacaat tataagctgt tt ttatatat gtgaaataaa agtagaataa acacaaaaaa 1680
aaaaaaaaaa aaaaaaaaaa aa                                     1702

```

&lt;210&gt; 372

&lt;211&gt; 585

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(585)

&lt;223&gt; 3' terminal sequence. oncogene tc21 (TC21) gene.

&lt;400&gt; 372

```

gtaggcagta tgattccaaa agttaaaaat tatttcacaa cctgtagctt cagcttggca 60
aacagcttag attccaaaac tgattcatct ctattaaaat gtaagcactt aaaaaaagag 120
catgtctgtg tatatagaca tat atttttaa aggaatcaga taatctttga agcagcctta 180
gtgtttcctt taaatttgtc tggaaatgac cattgtatta gcttcacaga aaggactagc 240
cagcttcttc gtctaaggct aacatggtga tcatttgtct aaggctagaa aggtaccaac 300
aagatgtaaa ctgaggagag aaagagaaga tgagggcttt tcctggccgt tggtagctaa 360
aactgaaggg attctagaaa atgacacaaat ggcagccttt cntgtctttt tctttccgtg 420
ttggttcnng tgaaggagga cattcctggc cctggaaatt tccnggataa cccggacaag 480
ttcatgggaa agcttgatct acattcatcc taatccttgc cggatgccnc catgtatgtt 540
acctaagctg ccggcaacgg tngcctctnc cggggtaccg gcc ng                    585

```

&lt;210&gt; 373

&lt;211&gt; 451

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(451)

&lt;223&gt; 5' terminal sequence. oncogene tc21 (TC21) gene.

&lt;400&gt; 373

```

gattcttaca caaagcagtg tgtgatagat gacagagcag cccggctaga tattttggat 60

```

237/292

```

acagcaggac aagaagagtt tggagccatg agagaacagt atatgaggac tggcgaaggc 120
ttcctgttgg tcttttcagt cacagataga ggcagttttg aagaaatcta taagtttcaa 180
agacagattc tcagagtaaa ggatcgtgat gagttcccaa tgattt taat tggtaataaa 240
gcagatctgg atcatcaaag acaggtaaca caggaagaag gacaacagtt agcacggcag 300
cttaaggtaa catacatgga ggcacagca aagattagga tgaatgtaga tcaantttcc 360
atgaacttgt ccgggttatc aggaaatttc aagancagga atgtcctctt cacagaccac 420
acggaaagaa aagccagaaa gctg cattgt g 451

```

&lt;210&gt; 374

&lt;211&gt; 425

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(425)

<223> 3' terminal sequence. cd44 antigen (homing  
function and indian blood group system) (CD44)  
gene.

&lt;400&gt; 374

```

gaagatcgaa gaagtacaga tatttattat gaatcagttt aaaccctttt gtgcctctga 60
caaagtaact ttaaaaaatt atactgatca aaggactgat ccagggttta atatttcaa 120
aacacagata aatagtttac tacagataaa tagcttcacc c ttgggtgtc ctccagaag 180
catctgaaaa atttctagag ggggtctgtt gaagatgtgt aactagtaca cccaacccc 240
caacctcagt ggaaagcaat gccagggat taggctatgg aagggcaaaa tggaccatt 300
caaatttcct ccaggggacc aggcctatt aaccctggga aatgtcctta gctggtggg 360
gaaaggttgg cgattcagga atacatatgt gtagtttttg ttagaagcca tccatagcac 420
accg 425

```

&lt;210&gt; 375

&lt;211&gt; 478

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(478)

<223> 5' terminal sequence. cd44 antigen (homing  
function and indian blood group system) (CD44)  
gene.

&lt;400&gt; 375

```

ggcgttccag ttcccacttg gaggccttc atccctcggg tgtgctatgg atggcttcta 60
acaaaaacta cacatatgta ttcctgatcg ccaacct ttc cccaccagc taaggacatt 120
tcccagggtt aatagggcct ggtccctggg aggaaatttg aatgggtcca ttttgccctt 180
ccatagccta atccctgggc attgctttcc actgaggttg ggggttggg tgtactagt 240
acacatcttc aacagacccc ctctangaaa tttttcagat gcttctggga gacacccaaa 300
ggggaaagct atttactgt agtaaaactat ttatctgtgt ttttgaaata ttaaaccctg 360
gatcagtcct ttgatcagta taaattttt aaagttactt ttgtcagagg caccaaagg 420
tttaaaactga ttcataaata aatatcngga cttoctcgat cttccaaaa aaaaaaaa 478

```

238/292

<210> 376  
<211> 1794  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(1794)  
<223> cd44 antigen (homing function and indian  
blood group system) (CD44) gene.

<400> 376  
ccgcgcgcct ccgttcgctc cggacacccat ggacaagttt tgggtggcacg ca gcctgggg 60  
actctgcctc gtgccgctga gcctggcgca gatcgatttg aatataacct gccgctttgc 120  
aggtgtattc cactgtggaga aaaatggctg ctacagcatc tctoggacgg aggccgctga 180  
cctctgcaag gctttcaata gcaccttgcc cacaatggcc cagatggaga aagctctgag 240  
catcggattt gagacctgca ggtatgggtt c atagaaggg catgtgggtga ttccccggat 300  
ccaccccaac tccatctgtg cagcaaacaa cacaggggtg tacatcctca catacaacac 360  
ctcccagtat gacacatatt gcttcaatgc ttcagctcca cctgaagaag attgtacatc 420  
agtcacagac ctgcccattg cctttgatgg accaattacc ataactattg ttaaccgtga 480  
tggcaccgcg tatgtccaga aaggagaata cagaacgaat cctgaagaca tctaccccag 540  
caaccctact gatgatgacg tgagcagcgg ctccctcagt gaaaggagca gcacttcagg 600  
aggttacatc ttttacacct tttctactgt acaccccatc ccagacgaag acagtccctg 660  
gatcaccgac agcacagaca gaatccctgc taccagagac caagacacat t ccaccccag 720  
tgggggggtcc cataccactc atggatctga atcagatgga cactcacatg ggagtcaaga 780  
aggtggagca aacacaacct ctggtcctat aaggacaccc caaattccag aatggctgat 840  
catcttgcca tccctcttgg ccttggtctt gattcttgca gtttgcattg cagtcaacag 900  
tcgaagaagg tgtgggcaga agaaaaagct agtgatcaac agtggcaatg gagctgtgga 960  
ggacagaaag ccaagtggac tcaacggaga ggccagcaag tctcaggaaa tgggtgcattt 1020  
ggtgaacaag gactcgctcag aaactccaga ccagtttatg acagctgatg agacaaggaa 1080  
cctgcagaat gtggacatga agattgggtt gtaacaccta caccattatc ttggaaagaa 1140  
acaaccgttg gaaacataac cattacaggg agctgggaca cttaacagat gcaatgtgct 1200  
actgattgtt tcattgcgaa tcttttttag cataaaattt tctactcttt ttgttttttg 1260  
tgttttgttc tttaaagtca ggtccaattt gtaaaaacag cattgctttg taaattaggg 1320  
cccaattaat aatcagcaag aatttgatcg ttcagttcca cttg gaggcc ttcacccctg 1380  
ggtgtgctat ggatggcttc taacaaaaac tacacatatg tattcctgat cgccaacctt 1440  
tccccacca gctaaggaca tttcccaggg ttaatagggc ctggtccctg ggaggaaatt 1500  
tgaatcggtc catcttgccc ttcataagcc taatccctgg gcattgcttt ccactgaggt 1560  
tgggggtgac tagttacac a ttttcaacag accccctcta gaaatttttc agatgcttct 1620  
gggagacacc aaagggtgaa gctatttatc tgtagtaaac tatttatctg tgtttttgaa 1680  
atattaaacc ctggatcagt cctttgatca gtataattt ttaaagttac tttgtcagag 1740  
gcacaaaagg gtttaaactg attcataata aatatctgta cttcttcgat cttc 1794

<210> 377  
<211> 452  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(452)  
<223> 3' terminal sequence. cyclin -dependent  
kinase inhibitor 3 (cdk2 -associated dual  
specificity phosphatase) (CDKN3) gene.

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&lt;400&gt; 377

```
ttttgtcaat aaaacttttag gaatatctgc acatgtacat ttacattcaa gttgataaca 60
ctgggtgggtt cattttcaata caaattatgc tagagaactg acatttcaga catggtcata 120
tatatgctat ttgaattcct ttatcttcga tacagatctt gattgtgaat ctc ttgatga 180
tagatgtgca gctaatttgt cccgaaactc atgaagataa ttgtattgct tgatggctcg 240
tattgccccg gatcctctta ggtctcgag gctgtctatg gcttgctctg gtgatattgt 300
gtcagacagg tatagtagga gacaagcagc tacaagacaa gatctcccaa gtcctccata 360
gcagtgtatt aagggttttc cggtaatttt t aaggcagggt tgtaagcnc tccattattt 420
cacagcagct ggccatgten ggagtccccc ca 452
```

&lt;210&gt; 378

&lt;211&gt; 472

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(472)

<223> 5' terminal sequence. cyclin -dependent  
kinase inhibitor 3 (cdk2 -associated dual  
specificity phosphatase) (CDKN3) gene.

&lt;400&gt; 378

```
ggcacgagcg gcaactggtc tcgacgtggg ggggccanga ctgaagccca ngnttcaata 60
caaacaagtg agtttgactc atcagatg aa gagcctattg aagatgaaca gactccaatt 120
catatatcat ggctatcttt gtcacgagtg aattgttctc agtttctcgg tttatgtgct 180
cttccagggt gtaaatttaa agatgttaga agaaatgtcc aaaaagatac agaagaacta 240
aagagctgtg gtatacaacg acatatttgt tttctgcacc agaggggaac tgtcaaaaata 300
tagagtccca aaccttctgg atctctacca gcaatgtgga attatcacc atcatcatcc 360
aatccgcaga tggagggact cctgacatag ccagctgctg tgaaataatg gaagagctta 420
caacctgcct taaaaattac cgaaaaacct taatacactg ctatggagga ct 472
```

&lt;210&gt; 379

&lt;211&gt; 639

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(639)

<223> cyclin-dependent kinase inhibitor 3  
(cdk2-associated dual specificity phosphatase)  
(CDKN3) gene.

&lt;400&gt; 379

```
atggagccgc ccagttcaat acaacaagtg gagtttgact catcagatga agagcctatt 60
gaagatgaac agactccaat tcatatatca tggctatctt tgtcacgagt gaattgttct 120
cagtttctcg gtttatgtgc tcttccagggt tgtaaattta aagatgttag aagaaatgtc 180
caaaaagata cagaagaact aaagagctgt ggtatacaag acatatttgt tttctgcacc 240
agaggggaac tgtcaaaaata tagagtccca aaccttctgg atctctacca gcaatgtgga 300
attatcacc atcatcatcc aatcgcatg ggagggactc ctgacatagc cagctgctgt 360
gaaataatg aagagcttac aacctgcctt aaaaattacc gaaaaacctt aatacactgc 420
```



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tatggaggac ttgggagatc ttgtcttgta gctgcttgt c tcctactata cctgtctgac 480  
acaatatcac cagagcaagc catagacagc ctgcgagacc taagaggatc cggggcaata 540  
cagaccatca agcaatacaa ttatcttcat gagtttcggg acaaattagc tgcacatcta 600  
tcacaaagag attcacaatc aagatctgta tcaagataa 639

&lt;210&gt; 380

&lt;211&gt; 487

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(487)

<223> 5' terminal sequence. max-interacting  
protein 1 (MXI1) gene.

&lt;400&gt; 380

aagtggcgac tggaacagct gcagggtcct caggagatgg aacgaatacg aatggacaga 60  
attggatcaa ctatttcttc agatcgttct gattcagagc gagaggagat tgaagtggat 120  
gttgaaagca cagagttctc ccatggagaa gtggacaata taagtaccac cagcatcagt 180  
gacattgatg accacagcag cctgccgagt attgggagtg acgagggtac tccagtgcc 240  
gtgtcaaaact ttcatctact tcatagaacc cagcatgaca taacagtgc gggaaaatat 300  
tcaatgggccc attcatacaa acaatctctt aaattgggtt catgatgcag tctcctcttt 360  
aaaacaaaac aaaacaaaac aaactatact tgaacaaaag ggtcagagga ctgttttaag 420  
caatacttag caaaagtggg cagctcccaa gagacaattt cagatttcat ttggaaatcc 480  
catttta 487

&lt;210&gt; 381

&lt;211&gt; 2416

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2416)

&lt;223&gt; max-interacting protein 1 (MXI1) gene.

&lt;400&gt; 381

agattatgat cgcctgaggg ccctctccta cccagatacc gatgttatac tgatgtgttt 60  
ttcctttttt tttttttttt ttaagtaat taagggtagt taaattattt aaagtataca 120  
aagtccaaac agccaggggt aaggtctcca agaggccttc ccagggttaag ggagtgcgga 180  
gaggcccccg tcgccaccgc cgtgcccac ggagcgggtg aagatgatca acgtgcagcg 240  
tctgtctggag gctgccgagt ttttgagcgc ccgggagcga gagtgtgaac atggctacgc 300  
ctcttcattc ccgtccatgc cgagcccccg actgcagcat tcaaagcccc cacggagggtt 360  
gagccgggca cagaacacac gcagcgggac gagcaacacc a gcaactgcc aacagatctac 420  
acacaatgag ctggaaaaga atcgacgagc tcatctgcgc ctttgtttag aacgcttaaa 480  
agttctgatt ccactaggac cagactgcac ccggcacaca acacttggtt tgctcaacaa 540  
agccaaagca cacatcaaga aacttgaaga agctgaaaga aaaagccagc accagctcga 600  
gaatttgga cgagaacaga gattttttaa gtggcgactg gaacagctgc aggttcctca 660  
ggagatggaa cgaatacgaa tggacagcat tggatcaact atttcttcag atcgttctga 720  
ttcagagcga gagagagatt aagtggatgt tgaaagcaca gagttctccc atggagaagt 780  
ggacaatata agtaccacca gcacagtgat cattgatgac cacagcagcc tgccgagtat 840  
tgggagtgac gaggggttact ccagtgccag tgtcaaactt tcattcactt catagaaccc 900

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```

agcatgacat aacagtgcag ggcaaaatat tcactgggcc aattcaatac aaacaatctc 960
ttaaattggg ttcatgatgc agtctctctt ttaaaacaaa acaaaacaaa acaaaactat 1020
acttgacaaa aagggtcaga ggacctgtat ttaagcaaa t acttagcaaa aagtggggca 1080
gagctcccaa ggagaacaaa tattcagaat attcatattg gaaaaatcac aatttttaat 1140
ggcagcagaa aacttgtgtg aaattttctt gatttgagtt gattgagaag aggacattgg 1200
agatgccatc ctctttctct tttctogttt gtcatacta cattgagtag acacatttaa 1260
ggatgggggt atg aaccctt cctgagcttt atggtcctaa aagcaaaata aaaactattc 1320
gaatgaaaag acaagaaaat caggtattaa tcttgatag ctaataatga gctattaaaa 1380
ctcagcctgg gacagtttat catgaagcct gtggatgac aatcctttat tattattttt 1440
tttttttgaa aaaagctcat ttcatgctct gcaaaaggag agactcccat ga agcctttt 1500
gaaagggatc atcatgcagc tcaactttct gttggattcc atgctaagca agctaaccctt 1560
atcctgcatt gttagcacta ggcacccagc tgccacctct ccatcctgct gcccttaggc 1620
cacatgggag cagtccatgc atgacagcct ctatcctaca aggcctatga gtatggattg 1680
gggggggcaa aaggaaaaag ctcatg tgc ctctttgtct gcgtgggtca gaagagtgtg 1740
gcacgcagat tagcaggcca aggtctgagc cacagcagca tttttatttc agattttgat 1800
aactgtttat atgtgttgaa aacaaaaatg acatcttttt aaagcttatc cataaaaaaa 1860
aatagatgtc ttttatagtg gaaaaacaca tggggaaaaa aatcatctat ttgatgcag 1920
catttgataa tgataaaaaca cctcacacct cactctttat agtgcacaaa atgaatgagg 1980
tctgggctag gtagaaaaag ggtcaatgct atttttgttt ttagaatcat taccttttac 2040
cagcttttaa ccactctgata tctatagtag acacactatc atagttaaca tagttaagtt 2100
cagcacttgt ctcattttaa tgtaaagatt tgcttcatt ttctacagg cagtctctct 2160
cttcctcaca gtcccactgt gcagggtgcta ttgttactct tacgaatatt ttcagtaatg 2220
ttattttctt ctaagtgaag tttctagcct gcactttgat gtcatgtgtt ccttttgtct 2280
ttcaaaactcc aagggtcccc tgtggccctc tcccttacc tggaaggcc tcttgagac 2340
cttaccctg gctgt ttgga ctttgtatac tttaaataat ttaactacc ttaattactt 2400
aaaaaaaaaa aaaaaa 2416

```

&lt;210&gt; 382

&lt;211&gt; 378

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(378)

&lt;223&gt; 3' terminal sequence. homeo box a5 (HOXA5) gene.

&lt;400&gt; 382

```

tttttttttt ttgttatagt tacttcaagt aacacagctt gttcatata aataagttaa 60
aacatctatt ttttttcaag acaaagccat tcaggacaaa gagatgaaca gaaagcagat 120
ctacttatac aggcgc tata atggcaataa acaggctcat gattaaaaga tgaattaggg 180
caacgagaac agggcttctt cacagaagga acacaaggga gtttcagaaa gtcaccttag 240
tactgacact acgcgggcat cgctaaatac tgctcagtag tttaaacgct cagatactca 300
gggacggaag gccctccctt gcccgggnc atnctcatg gcttttcagc ttattatc tt 360
ttttccactt caatcncc 378

```

&lt;210&gt; 383

&lt;211&gt; 439

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

242/292

<221> misc\_feature  
<222> (1)..(439)  
<223> 5' terminal sequence. homeo box a5 (HOXA5) gene.

<400> 383  
aaatcaagca cacatantan aaaacaaatg agctcttatt ttgtaaactc attttgcggt 60  
cgctatccaa atggcccgga ctaccagttg cataattatg gagatcatag ttccgtganc 120  
gagcaattca gggactcggc gagcatgcac tccggcaggt acggctacgg ctacaatggc 180  
atggatctca gcgtcggcng ctgngctcc ngcacttttg ctccggagag cgcgcccga 240  
gctacgtnc agcgcacgc ggcncactcc aagcccaggt acagcnagcc ggccacgtcc 300  
acgcactctn cctcanncg atccgctgcn ctgctccgnc gtnggccct tgcgccngga 360  
ancgacanna ccaangggcg gaaaaactcc cttaaggca a ctccagcngg cgctcgggc 420  
cgacngccgg aagcaccca 439

<210> 384  
<211> 813  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(813)  
<223> homeo box a5 (HOXA5) gene.

<400> 384  
atgagctctt atttgtaaa ctcatcttgc ggtcgctatc caaatggccc ggactaccag 60  
ttgcataatt atggagatca cagttccgtg agcagagcaat tcagggactc ggcgagcatg 120  
cactccggca ggtacggcta cggctacaat ggcattggtc tcagcgtcgg ccgctcgggc 180  
tccggcact ttggtccgg agagcgcgcc cgcagctacg ctgccagcgc cagcgcggcg 240  
cccgcgcagc ccaggtacag ccagccggcc acgtccacgc actctcctca gcccgatccg 300  
ctgccctgct ccgccgtggc cccctcgccc ggcagcgcgc cgcaccacgg cgggaaaaac 360  
tccttaagca actccagcgg cgctcggcc gacgccggca gc acccacat cagcagcaga 420  
gagggggttg gcacggcgtc cggagccgag gaggacgcc ctgccagcag cgagcaggcg 480  
agtgcgcaga gcgagccgag cccggcgccg cccgcccaac cccagatcta cccctggatg 540  
cgcaagctgc acataagtca tgacaacata ggcggcccgg aaggcaaaaag ggcccggacg 600  
gcctacacgc gctaccagac cctggagctg gagaaggagt tccacttcaa ccgttacctg 660  
acctgcagaa ggaggattga aatagcacat gctctttgcc tctccgagag acaaattaaa 720  
atctggttcc aaaaccggag aatgaagtgg aaaaaagata ataagctgaa aagcatgagc 780  
atggccgcgg caggaggggc cttccgtccc tga 81 3

<210> 385  
<211> 447  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(447)  
<223> 3' terminal sequence. x-box binding protein 1 (XBP1) gene.

<400> 385

243/292

```
gcattgtacc ttttaattgc atgggtagtt ttaaataaat ggagaaagca cttttcagaa 60
gctacactag caggaaaaaa ttccatcaag catttacata gttaaatttct ataatttcac 120
aaaagattct tgatcttact tgaagtatac atgagggaaa gagccccctc agcagggtgtt 180
cccgttgctt acagaagcaa actaaaggac ctaaaactgg aggcaagcca ggatgc caaa 240
aagggggaag agaaatgata aagaaccatt cataaattcc atgtctactt caagacattt 300
gtctaatac cttacataa taagtatttt agggaaaact accacccttt taagataaaa 360
gtacaatctt aaaagctgta gttctcaatt atagtaatat ttctacttc cagtaatatg 420
tctcaatacc ttggactgct ggatgtc 447
```

&lt;210&gt; 386

&lt;211&gt; 462

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(462)

<223> 5' terminal sequence. x-box binding protein  
1 (XBP1) gene.

&lt;400&gt; 386

```
aagaacctgt agaagatgac ctcgttccgg agctgggtat ctcaaactctg ctttcatcca 60
gccactgccc aaagccatct tcctgcctac tggatgctta cagtgactgt ggatacgggg 120
gttccctttc cccattcagt gacatgtcct ctctgcttgg tgtaaaccat tcttggggagg 180
acacttttgc caatgaactc tttcccca gc tgattagtgt ctaaggaatg atccaatact 240
gttgcccttt tccttgacta ttacactgcc tggaggatag cagagaagcc tgtctgtact 300
tcattcaaaa agccaaaata gagagtatac agtcctagag aattcctcta tttgttcaga 360
tctcatagat gacccccagg tattgtcttt tgacatccca agcagtcocaa ggtattggag 420
acatattact gggaagtaaa gaaatattac tnataattgg ag 462
```

&lt;210&gt; 387

&lt;211&gt; 1836

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1836)

&lt;223&gt; x-box binding protein 1 (XBP1) gene.

&lt;400&gt; 387

```
ggcgctgggc ggctgcggcg cgcggtgcgc ggtgcgtagt ctggagctat ggtggtggtg 60
gcagccgcgc cgaacccggc cgacgggacc cctaaagttc tgcttctgtc ggggcagccc 120
gcctccgcgc ccggagcccc gccgggccag gccctgccgc tcatggtgcc agcccagaga 180
ggggccagcc cggaggcagc gagcgggggg ctgccccagg cgcgcaagcg acagcgcctc 240
acgcacctga gccccgagga gaaggcgctg aggaggaaac tgaaaaacag agtagcagct 300
cagactgccca gagatcgaaa gaaggctcga atgagtgcgc tggaacagca agtggtgat 360
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ggcctttagt ttgagaacca ggagttaaga cagcgcttgg ggatggatgc cctggttgct 480
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gcagactca gactacgtgc acctctgcag caggtgcagg ccagttgtc acccctcag 600
aacatctccc catggattct ggcggtattg actcttcaga ttcagagtct gatatacctgt 660
tgggcattct ggacaacttg gaccagtc tgttcttcaa atgcccttc ccagagcctg 720
```

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ccagcctgga ggagctccca gaggtctacc cagaaggacc cagttcctta ccagcctccc 780
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ttgaccacat atataccaa g cccctagtct tagagatacc ctctgagaca gagagccaag 900
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tctaaggaat gatccaatac tgttgccctt ttcttgact attacactgc ctggaggata 1260
gcagagaagc ctgtctgtac ttattcaaa aagc caaat agagagtata cagtcctaga 1320
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caattaaaag gtacaatgca aaaaaaaaa aaaaaa 1836

```

&lt;210&gt; 388

&lt;211&gt; 433

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(433)

<223> 3' terminal sequence. tumor necrosis factor,  
alpha-induced protein 3 (TNFAIP3) gene.

&lt;400&gt; 388

```

tttttcttaa ataatttatt ttttaatgtt gactcttgtg aaaagttaca tttatttaga 60
aaaacttgaa gaaatccaac aaagaatagg tggctttcta ttagggacaa ttaaagtgtc 120
aaatttcaaa tactttttat aataagtata aataattact ttttttcaca ttaagaatgg 180
aaataatgat caacacaana tattaaagata tcaactttaa gagaattaga tgaaaacact 240
gaagtttatt tngtatacct tggaaangaa ttataaagat tctgtctgga aaaactt agg 300
gggctctaag gggaaagttg tgcctaatag tatgagtaaa ggctgtgtag agttatggat 360
cacaaatatt ttcaggcctt aagtacagac cccnnaatg gcagccttta tcncgggga 420
aatgcattt ccc 433

```

&lt;210&gt; 389

&lt;211&gt; 206

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(206)

<223> 5' terminal sequence. tumor necrosis factor,  
alpha-induced protein 3 (TNFAIP3) gene.

&lt;400&gt; 389

245/292

```
ctcaaccagc tgccttttta aaggga gctc tagtcctttt tgtgtaattc actttattta 60
ttttattaca aacttcaaga ttatttaagt gaagatattt cttcagctct ggggaaaatg 120
ccacagtgtt ctctgagag aacatccttg ctttgagtca ggctgtgggc aagttcctga 180
ccacagggag taaatngnn cctctt 206
```

&lt;210&gt; 390

&lt;211&gt; 4426

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(4426)

<223> tumor necrosis factor, alpha -induced protein  
3 (TNFAIP3) gene.

&lt;400&gt; 390

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agcacaatgg ctgaacaagt ccttcctcag gctttgtatt tgagcaatat gcggaaaagct 120
gtgaagatac gggagagaac tccagaagac atttttaaac ctactaatgg gatcattcat 180
catttttaaaa ccatgcaccg atacacactg gaaatgttca gaacttgcca gtt ttgtcct 240
cagtttcggg agatcatcca caaagccctc atcgacagaa acatccaggc caccctggaa 300
agccagaaga aactcaactg gtgtcgagaa gtccggaagc ttgtggcgct gaaaacgaac 360
ggtgacggga attgcctcat gcatgccact tctcagtaca tgtggggcgt tcaggacaca 420
gacttggtac tgaggaaagg gctgttcagc a cgctcaagg aaacagacac acgcaacttt 480
aaattccgct ggcaactgga gtctctcaaa tctcaggaat ttgttgaaac ggggctttgc 540
tatgatactc ggaactggaa tgatgaatgg gacaatctta tcaaaatggc ttccacagac 600
acacccatgg cccgaagtgg acttcagtac aactcactgg aagaaatata catatttgc 660
ctttgcaaca tcttcagaag gccaatcatt gtcatttcag aaaaatgct aagaagttg 720
gaatcagggt ccaatttgcg ccctttgaaa gtgggtggaa tttacttgcc tctccactgg 780
cctgccagg aatgctacag atacccatt gttctcggct atgacagcca tcattttgta 840
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gaccggggaa gatttgaaga cttaaaagt cactttttga cagatcctga aaatgagatg 960
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cccaaccaga ggatggggcc tggggccac cggggtgagc ctgccccga agaccccccc 2340
aagcagcgtt gccgggcccc cgctgtgat cattttggca atgccaagtg caacggctac 2400
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tgcaacgaat gctttcagtt caagcagatg tatggctaac cggaaacagg tgggtcacct 2460
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gctgccactg caacagtggg cttaaggggtg tctgagcagg agaggaaaga taagctcttc 2580
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&lt;210&gt; 391

&lt;211&gt; 440

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(440)

<223> 3' terminal sequence. serum response factor  
(c-fos serum response element-binding  
transcription factor) (SRF) gene.

&lt;400&gt; 391

```

ttttttgtg cacaataatg atacatttat tgaaagagta tttttttttt aatacaaaaag 60
aaagctctgt acataggact gtgacctgt ccactattcc tgggtcagca tcccagggga 120
agtagaaacc actgacatac aactcacat tcaagcacac aactcactc aggcgcacac 180
accacacac acatacccca gagccacga ggaagggaaa caccaagggt cgctgcacat 240
aaaaatatca cctcaactca tccctgacac acgcatgtcc tcccaaggcc acgtcacac 300
aacacacatt ataagcatt tgcctgattc actcactngg gtctgtcttt tgtgggaagg 360
agaggaagaa ttcatcaaag gtctcctccc catgggtngg gggagtggg agtgagtgag 420
tgatggtgga gtgaaacaag

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<210> 392  
<211> 471  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(471)  
<223> 5' terminal sequence. serum response factor  
(c-fos serum response element-binding  
transcription factor) (SRF) gene.

<400> 392  
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tttttaaat aagacaaaaa gccttgaaga aaatgacttt atttttctaa gtgtaacctc 180  
agtatttatg taatttgtag aggggccatg ccacncccc tctccccct ttngtnaga 240  
ccttgagggt gggccagcat aggggggagg gtcttttacc ctgtgtcaga gcctaccttc 300  
accacctata tccagaaggg gagctttttc agaaacaggg cagcagtggg gtgaaatttt 360  
cttaaccct aagactgcct tcagtaagga acaagctggc ttctgtgatt aggtgaaggg 420  
atgggggaag attttaatgc acagccta gt tatcaagggg atgatttgcc g 471

<210> 393  
<211> 4201  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(4201)  
<223> serum response factor (c-fos serum response  
element-binding transcription factor) (SRF) gene.

<400> 393  
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gcagacggac agggggcgct gcgcgggcc tggggcaacc cgggccac ag gggcaggaaa 180  
gtgaggggcc aggtcggccc gggcgtgcag gggccccggg ttgcagcgg cggccgcggc 240  
agcgatagcg gcactagcag cagcgggagt gccgggttga gccgggaagc cgatggcggc 300  
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gttaccgacc caagctgggg ccgcgg cggc tctgggccc ggctcggccc tggggggcag 420  
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cagcaaggag aagacgggca tcatgaagaa ggcctatgag ctgtccacgc tgacagggac 900  
acagggtctg ttgctggtgg ccagtgcagc aggccatgtg tatacctttg ccaccgaaa 960  
actgcagccc atgatcacca gtgagaccgg caaggcactg attcagacct gcctcaactc 1020  
gccagactct ccaccccggt cag accccac aacagaccag agaatgagtg cactggctt 1080  
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cacactgaag cggcggttca cagtcaccaa cctgcggggt acaacctcca ccatccaaac 1200
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g 4201

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&lt;210&gt; 394

&lt;211&gt; 563

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

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<220>  
<221> misc\_feature  
<222> (1)..(563)  
<223> 3' terminal sequence. sry (sex determining  
region y)-box 9 (campomelic dysplasia, autosomal  
sex-reversal) (SOX9) gene.

<400> 394  
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tgaaacaaac aaaacacgaa cacaaccaa agcttttacc taaagacaaa atatgattta 180  
aatgccagggt ttcttaagtt acaga agtat ctttttaaaa agatctgctt ttatacagaa 240  
attgaaggat gccatattat gagtgtttaa agattttatt ctactgactt ctaaaactgt 300  
taatatatct ttttttaaata aaaaaaaaaa gtttgctgtc ttttttaaaa agcaatcctc 360  
aaactctcta gccacagcag taattaagat taaggctctgt cagtgggctg atccctcca 420  
ggtagcctcc ctactccaa gagaagatgc ngagaaatat gggatggaca catgcctgca 480  
tgtttttggtg nccaacaca cacanacca nacacacnca caatataagg cngccccaag 540  
gtctntggcc gaaancctgg caa 563

<210> 395  
<211> 3936  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(3936)  
<223> sry (sex determining region y) -box 9  
(campomelic dysplasia, autosomal sex -reversal)  
(SOX9) gene.

<400> 395  
ggagagccga aagcggagct cgaaactgac tggaaacttc agtggcgcg agactcgcca 60  
gtttcaaccc cgaaacttt tctttgcagg aggagaagag aaggggtgca agcgcccca 120  
cttttgctct ttttctccc ctctctctcc tctccaattc gctcccccc acttgagcgc 180  
ggcagctgtg aactggccac ccgcgcctt cctaagtgtc cgccgcgta gccgc cgac 240  
gcgccagctt ccccgggagc cgcttgcctc gcatccgggc agccgagggg agaggagccc 300  
gcgcctcgag tcccagagcc gccgcggtt ctgccttcc ccggccacca gcccctgcc 360  
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ggcctgtccg gcgccccag cccaccatg tccg aggact ccgcgggctc gccctgcccg 480  
tcgggctccg gtcgggacac cgagaacacg cgccccagc agaacacgtt ccccaagggc 540  
gagcccgatc tgaagaagga gagcgaggag gacaagttcc ccgtgtgcat ccgcgagggc 600  
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ggctccagca agaacaagcc gcacgtcaag cggcccatga acgccttcat ggtgtgggcg 720  
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aagacgctgg gcaagctctg gagacttctg aacgagagcg agaagcggcc cttcgtggag 840  
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cgcgaggaga gtcgggtgaa gaacgggcag gcggaggcag aggaggccac ggagcagacg 960  
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gagctgagca gcacgtcat ctccaacatc gagaccttcg atgtcaacga gtttgaccag 1260  
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ggcagctacg gcatcagcag caccgcgcc acccgcgca gcgcgggcca cgtgtggatg 1380  
tcaaagcagc aggcgcgcgc gccacccccg cagcagcccc cacaggcccc gccggccccg 1440

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caggcgcccc cgcagccgca ggcggcgccc ccacagcagc cggcggcacc cccgcagcag 1500
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ttgtttacaa taaatatata tt gcattaaa aagaaa 3936

```

&lt;210&gt; 396

&lt;211&gt; 204

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(204)

<223> 3' terminal sequence. cadherin 15,  
m-cadherin (myotubule) (CDH15) gene.

&lt;400&gt; 396

```

tttttttttt tttttttttt tttttttttt ttttttttca ttcagattta cccaggaggt 60
tgctgtcttt canacaaaga tgaggttcac tgnnaggagg caaaggtggg actaggagg 120

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tgacccgcat gggccagatn ggagagaaac ttttcccacc cgggcagaag gggcctcttc 180  
ctggccgccc catccanact cagg 204

<210> 397  
<211> 458  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(458)  
<223> 5' terminal sequence. cadhe rin 15,  
m-cadherin (myotubule) (CDH15) gene.

<400> 397  
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tgcccacccag ccccttgagc atcgccgact tcatcaatga tggcttgga g gctgcagata 180  
gtgacccacag tgtgcgcct tacgacacag ccctcatcta tgactacgag ggtgacggct 240  
cgggtggcggg gacntgagct ccatcctgtc cagccagggc gatgaggacc aggactacga 300  
ctacctcaga gactgggggc cccgcttcgc ccggctggca gacatgtatg ggcacccgtg 360  
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gcactgctac ccagacacag aggccggaca gcctgan 458

<210> 398  
<211> 2833  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(2833)  
<223> cadherin 15, m-cadherin (myotubule) (CDH15)  
gene.

<400> 398  
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gcctctgcct gtctttgggg gtt cctggat ggaggaggcc caccacctg taccctggc 180  
gccgggcgccc tgccctgagc cgcgtgcgga gggcctgggt catccccccg atcagcgtat 240  
ccgagaacca caagcgtctc ccctaccccc tggttcagat caagtcggac aagcagcagc 300  
tgggcagcgt catctacagc atccagggac ccggcgtgga tgaggagccc cggggcgtct 360  
tctctatcga caagttcaca gggaaggtct tcctcaatgc catgctggac cgcgagaaga 420  
ctgatcgctt caggctaaga gcgtttgccc tggacctggg aggatccacc ctggaggacc 480  
ccacggacct ggagattgta gttgtggatc agaattgacaa ccggccagcc ttcctgcagg 540  
aggcgttcac tggccgcgtg ctggagggtg cagtcccagg cac ctatgtg accagggcag 600  
aggccacaga tggcagcagc cccgagacgg acaacgcagc gctgcggttc tccatcctgc 660  
agcagggcag ccccgagctc ttcagcatcg acgagctcac aggagagatc cgcacagtgc 720  
aagtggggct ggaccgcgag gtggtcgcgg tgtacaatct gacctgcag gtggcggaca 780  
tgtctggaga cggcctcaca g ccaactgcct cagccatcat cacccttgat gacatcaatg 840  
acaatgcccc cgagttcacc agggatgagt tcttcatgga ggccatagag gccgtcagcg 900  
gagtggatgt gggacgcctg gaagtggagg acagggacct gccaggctcc ccaaactggg 960  
tggccagggt caccatcctg gaaggcgacc ccgatgggca gttcaccatc cgcacggacc 102 0

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```

ccaagaccaa cgagggtgtt ctgtccattg tgaaggccct ggactatgag agctgtgaac 1080
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ccttctgtcc ggggtgggaa gagtctctct ccacggccc catgcgggtc acc tccctag 2760
tcccaccttt gctcctacc agtgaacctc atctttgtat gaaagacagc aacctcctgg 2820
gtaaatctga atg 2833

```

&lt;210&gt; 399

&lt;211&gt; 646

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence: primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(646)

<223> 3' terminal sequence. b-cell cll/lymphoma 2  
(BCL2) gene.

&lt;400&gt; 399

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tatctcacac tgtactttat tttctttcac aatattaact agacagacaa ggaaagttta 60
atggcaatgt gactttttcc aacaacacaa acaaagtgcc attata gcta atggtggcca 120
actggagact tactttacct taaccatgta aagtatcctt accgtatttt ttatgtgtac 180
agtgttcag aatatcagcc acctcttaaa agtatcaatc ttaaaaagag ccatggaagg 240
taaaagtatg aaaatcttga taacaaaagc tttaataca aaaacactta ttgtacactt 300
atttttattt aaacaaaaaa taac ccagat aactcaaaac aaaagcaaac cttggttgaa 360
aacttaagaa ggtataataa acaaaaccac caaaagaaag cttccccaaa agaaatgcaa 420
tccactgtca ctcttgcaaa ttctaccttg gagggaaaaa cttaatgaaa tgagctatct 480
ggaggggccca cggagatttt ccaaaagggt taggtgcatg gatttactca gtatctacnt 540
acagtcttat ttattaatag ctgaganttc ctgattgagc gagcctttcc atctccacca 600
gtgtcccccac ttctgtgcnc acttgggntg cagacaccct gtgttg 646

```

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<210> 400  
<211> 465  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(465)  
<223> 5' terminal sequence. b-cell cl1/lymphoma 2  
(BCL2) gene.

<400> 400  
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ttggtaggga catctgtttc taaatgttta ttatgtacaa tacagaaaaa aattttataa 1 20  
aattaagcaa tgtgaaactg aattggagag tgataataca agtcctttag tcttaccag 180  
tgaatcattc tgttccatgt ctttggacaa ccatgacctt ggacaatcat gaaatatgca 240  
tctcactgga tgcaaagaaa atcagatgga gcatgaatgg tactgtaccg gttcatctgg 300  
actgccccag aaaaataact tcaagcaaac atcctatcaa caacaagggt gttctgcata 360  
ccaagctgag cacagaagat gggaacactg gtggaggatg gaaaggctcg ctcaatcaag 420  
aaaattctga gactattaat aaataagact gtagtgtaga tactg 465

<210> 401  
<211> 419  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(419)  
<223> 3' terminal sequence. ests (EST W73386)  
gene.

<400> 401  
gaaggtcatt cttgcgatgg gtttattgca ggagatgatg gaccaaattgg ctctgacaca 60  
tgcacacgct cctgggcacg cctgctgcgn gtncgcttcc catga cccc agggccctct 120  
atgcctcccc cccagggcac cctgcccact tgccccact tcatgtacca ccaagccctt 180  
tccttttctg ggcaccactc ctgagcagcg tgaccagcgg cctccaagtg catgtggctc 240  
agaacataaa agcatcttca acattogtca ttgagccaaa cgaaacacag tgtttggtc 300  
aagagccggc gacactngca tcc ctatcca cagtggaac ctgcccttgg gcttngttga 360  
ccggaggatn ggccgctctt ccttgtcatc cagcancgg agcatgtatg tgcccaga 419

<210> 402  
<211> 568  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(568)  
<223> 3' terminal sequence. granzyme a (granzyme

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1, cytotoxic t-lymphocyte-associated serine  
esterase 3) (GZMA) gene.

&lt;400&gt; 402

```
tcatgcaaat tgattttatt tgtgaaaaga ttaagaagcc acagtanatg aaaggaaacg 60
gttattttaa ctgctccctt gatagt cata attatccagt tgagggtgtt ctttgagaga 120
agaatataga caccaggccc acgaggggtct ccgcatttat tttcaaggcc aaaggaagtg 180
acctctcgga aaacacctc gcacaacaaa gggcttccag aatctccatt gcacgagtct 240
cttccacctc ggagggttcc agcacaaccc atattcattc caatcacagg gttaaaatta 300
tagtgatttc gatcattgca gacttttctg tctatgatgg gtgatattga cttgcactca 360
gagtatcggg acctaatgat cactattggg gagtctgcc ccacctggc aacttggcac 420
atggttctct gntttcacat caatccccct ttttagggag atgaaggata gtcacatatn 480
tggttatttt ggctttttcc ggtcagctgt aaagttttaa ggtccc ctnc gcgtttgtg 540
gggcctagcc tggtagggga aanccttt 568
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&lt;210&gt; 403

&lt;211&gt; 878

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(878)

<223> granzyme a (granzyme 1, cytotoxic  
t-lymphocyte-associated serine esterase 3) (GZMA)  
gene.

&lt;400&gt; 403

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cagattttca ggttgattga tgtgggacag cagccacaat gaggaactcc tatagatttc 60
tggcatcctc tctctcagtt gtctgttctc tctgtctaatt toctgaagat gtctgtgaaa 120
aaattattgg aggaaatgaa gtaactctc attcaagacc ctacatggtc ctacttagtc 180
ttgacagaaa aaccatctgt gctggggctt tgattgcaaa agactgggtg ttgactgcag 240
ctactgtaa cttgaacaaa aggtcccagg tcattcttgg ggctcactca ataaccaggg 300
aagagccaac aaaacagata atgcttgta agaaagagtt tcc ctatcca tgctatgacc 360
cagccacacg cgaagggtgac cttaaaacttt tacagctgac ggaaaaagca aaaattaaca 420
aatatgtgac tatccttcat ctacctaaaa agggggatga tgtgaaacca ggaacctgt 480
gccaagtgc aggggtggggg aggaactcaca atagtgcac ttggtccgat actctgagag 540
aagtcaatat caccatcata gacagaaaag tctgcaatga tcgaaatcac tataatttta 600
acctgtgat tggaatgaat atggtttgtg ctggaagcct ccgaggtgga agagactcgt 660
gcaatggaga ttctggaagc ctttgttgt gcgaggtgt tttccgagg gtcacttct 720
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agaaacacct caactggata attatgacta tcaaggagc agtttaaata accgtttct 840
ttcatttact gtggcttctt aatcttttca caataaaa 878
```

&lt;210&gt; 404

&lt;211&gt; 191

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(191)

&lt;223&gt; 3' terminal sequence. v-fos fbj murine

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osteosarcoma viral oncogene homolog (FOS) gene.

&lt;400&gt; 404

```
gcagtgaccg tgctcctacc cagctctgct tcacagcgcc cacctgtctc cgcccctcgg 60
cccccgccc ggctttgcta accgccacga t gatgttctc gggcttcaac gcagactacg 120
aggcgctcatc ctcccgctgc agcagcgcggt ccccggccgg gataanctct ctttattaca 180
attaatcanc g 191
```

&lt;210&gt; 405

&lt;211&gt; 245

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(245)

<223> 5' terminal sequence. v-fos fbj murine  
osteosarcoma viral oncogene homolog (FOS) gene.

&lt;400&gt; 405

```
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tttttcattc aaattcactt tccacatgtc aaaagacctc aaggtagaaa aaaataaaat 120
aaaaatataa atatctgaga atccatctta ataaataaat taaaaacaca ataaaacggt 180
ttcatggaaa actgttaatg tcnngaacat tcagaccacc tcnacaatgn gtgntcngtn 240
anatt 245
```

&lt;210&gt; 406

&lt;211&gt; 489

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(489)

<223> 3' terminal sequence. interleukin enhancer  
binding factor 1 (ILF1) gene.

&lt;400&gt; 406

```
gcgncgcgct caccgaaggg ngnangtaga cagcgggtca gaggccgcct agagccggag 60
gacaccccaa atacaaacat accacggaga gacctgggat ctgagtttca aaagggcctg 120
tgataaaaaga ctgaatcttt ttccaaatga agtagaaatg gttctgtcgt tttaaacata 180
cacaatactt aggagacttg tt ttactcag agtggaatgt tttgccaggg acaaagtcaa 240
cacaaagaaa caaacaacaa aaaatagcca gaaagagaac agttaagtgc agctcgggtga 300
gtcccgccag ttcttcccg gcaactggctc gtccctgggt tctcaagggt ccatgcggcc 360
acagcgctccg tccacctgct cagcgagcc acatgctgaa atgggagggt ggataaaatt 420
catcaggcag ctgctgtaac acggaaatgt gcagatgcc a gagtagcttc gtctgaactt 480
gaacaagac 489
```

&lt;210&gt; 407

&lt;211&gt; 247

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence



&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(247)

<223> 5' terminal sequence. interleukin enhancer  
binding factor 1 (ILF1) gene.

&lt;400&gt; 407

```
tgttttcagc ctatggaatg atttcctttt gtctgtcttg ttcaagttca gacgaagcta 60
ctctggcatc tgcacatttc cgtgttacag cagctgcctg atgaa tttta tccacctcca 120
tttcagcatg tggctcgcgt ggacaggtgg acggacgctg tggccgcatg gaaccttgag 180
aaccagggga cgagccagtg ccgggaagga actgccggga ctaccganc tgcncctaac 240
tgttctc                                     247
```

&lt;210&gt; 408

&lt;211&gt; 3059

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(3059)

<223> interleukin enhancer binding factor 1 (ILF1)  
gene.

&lt;400&gt; 408

```
gcccccccc cagcctcct cccctcctcc cgcccgcgcg tgetcccccc cctcgccgcc 60
gctcgctcgc tcgcccggcg gctcgcgtc ggccccctcc ctacagctccg gtgcgcggcg 120
gccgacgacc cgcgccctgg gctcggcgcg gccaccggcg ccgcgcggga gcggcccggy 180
ggccctcagc caggcccatg gcggcgggcg ggcgcgctct cgggccgggc accacgcggg 240
cgcgggggcg gggcgccggg gccggggggc ggtcccccg ggcgctgggc cgtggggcgc 300
ctggagggcc gcgagttcga gtatctgat aagaagcgct cggtgaccat cggccgcaac 360
tcgtcgagg gctcgttga cgtgagcat ggccactcga gttcatctc ccggcgccac 420
ctcgagatct tcacgcccc ggcgggcgcg gccatggcg ggccgctccg gagctgcgc 480
ccgcgcagcc caggcccgac gccggcgggc acttctacct gcgctgcttg ggcaagaacg 540
gggtattcgt ggacggcggt ttccagaggc gcggggcgcc gccgctgcag ctgccgcgcg 600
tgtgcacatt caggttcccg agcacaaca tcaagataac gttcactgcc ctgtccagcg 660
agaagagaga gaagcaggag gcgtctgagt ctccagtga a ggccgtacag ccacacatct 720
cgccctgac catcaacatt ccagacacca tggcccacct catcagccct ctgccctccc 780
ccacgggaac catcagcgct gcaaactcct gcccctccag ccccgggga gcggggtctt 840
caggggtacaa ggtgggcoga gtgatgccat ctgacctcaa ttaatggct gacaactcac 900
agcctgaaaa tgaaaag gaa gttcaggtg gagacagccc gaaggatgat tcaaagccgc 960
cttactccta cgcgagctg atagttcagg cgattacgat ggctcccgac aaacagctca 1020
ccctgaacgg gatttataca cacatcacta aaaattatcc ctactacagg actgcggaca 1080
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agcggcagct accacaggcc atcaagcctg tcacctacac tgtggccacc ccagtgacca 1560
cctcgacctc ccagccaccc gtcgtgcaga cggttcacgt cgtccaccag atcccagcgg 1620
tgtcgtcac cagtgtggcc ggactggccc cagcgaacac gtacactgtc tctggacaag 1680
```

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```
ctgtggtcac cccggcagcc gtgctggccc ctcctaaggc agaggcccag gagaatggag 1740
accacagggg agtcaaagt aaagtagagc ctattcccgc cattg gccac gccacgctcg 1800
gcaactgccag ccgatcatt cagacggcac agaccacccc ggtccagacg gtgaccatag 1860
tacaacagggc acctctaggt caacaccagc taccaataaa aactgtaaca caaaacggca 1920
ctcacgtggc atcagtcccc actgcggtcc acggccaggt gaacaatgcc gcggcgagtc 1980
ctttgcacat gttggcaaca cagcatccg catcgccctc cctgcccaca aagcgccaca 2040
acggtgacca gccggagcag ccggagctga agcggatcaa gacagaagac ggcgagggca 2100
tcgtcattgc cctgagcgtg gacacgccac cggcagccgt aagggaagag ggtgtccaga 2160
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cggcctcccg ccagcactcg ggggtgcagg gccctgtggt tggacttcac ctctcagcac 2280
tgaaaaccca aaaccagct ggccttaaca ctcttaag acagaagtca cacttgaaca 2340
aaaccacac acaacaaaac ctgatttggg agacggtgtc tccactgagc acctgctggg 2400
ctgagcttct acctacgagt gaaactctgt cct cccgcga ggaccaggca tcgctgtgtg 2460
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aagaaacaac atagtattgt ttttgttttc agcctatgga atgatttctt tttgtctgtc 2760
ttgttcaagt tcagacgaag ctactctggc atctgcacat ttccgtgtta cagcagctgc 2820
ctgatgaatt ttatccacct ccatttcagc atgtggctcg cgtggac agg tggacggacg 2880
ctgtggcccg atggaacctt gagaaccag ggacgagcca gtgccgggaa ggaactgccg 2940
ggactcacgg agctgcactt aactgttctc tttctggcta tttttgttg tttgtttctt 3000
tgtgttgact ttgtccctgg caaaatttcc cactctgagt aaaacaagtc tcggaattc 3059
```

&lt;210&gt; 409

&lt;211&gt; 201

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(201)

<223> 3' terminal sequence. rho gdp dissociation  
inhibitor (gdi) alpha (ARHGDIA) gene.

&lt;400&gt; 409

```
ttttttttt tccttcaggg gcatttattt cccggtcaga aaagaagcag ggacaggcgc 60
ctctgcctga gcctggcaga cacaacacga agaccgggga tggggcgggg gaggcacagg 120
agacggctct cagcaatgtg tgcacttggc cccttgtttg ttctggctg ggtcagggaa 180
ggcctgccgn ggggtggtgg a 201
```

&lt;210&gt; 410

&lt;211&gt; 297

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(297)

<223> 5' terminal sequence. rho gdp dissociation  
inhibitor (gdi) alpha (ARHGDIA) gene.

&lt;400&gt; 410

258/292

ggcctctgct gccctttctg tgccccccag gttctatctc cccgtcacac ccgaggcctg 60  
gcttcaggag ggagcggana gccattctcc agggcccggtg gttgcccctg gacgtgtgcg 120  
tctgctgctc cggggtggan ctggggtgtg ggatgcacgg cctcgtgggg gccgggcccgt 180  
cctccagccc cgtgctccc tggccagccc cc ttgtcgtc gtcgggtccc tctaaccatg 240  
atgccttaac atgtggagtg tacctgtggg gcctcactaa gcctctaant cactgtg 297

&lt;210&gt; 411

&lt;211&gt; 1819

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1819)

<223> rho gdp dissociation inhibitor (gdi) alpha  
(ARHGDI A) gene.

&lt;400&gt; 411

cctgaaccgc gcggccgaac cctccgggtg cccgaccag gctaagcttg agcatggctg 60  
agcaggagcc cacagccgag cagctggccc agattgcagc ggagaacgag gaggatgagc 120  
actcgggtcaa ctacaagccc ccggcccaga agagcatcca ggagatccag gagctggaca 180  
aggacgacga gagcctgcga aagtacaagg agggccctgct gggccgctg gccgtttccg 240  
cagaccccac cgtccccaac gtcgtggtga ctggcctgac cctggtgtgc agctcggccc 300  
cgggcccctt ggagctggac ctgacgggag acctggagag cttcaagaag cagtcgtttg 360  
tgctgaagga ggggtgtggag taccggataa aaatctcttt ccgggttaac cgagagatag 420  
tgtccggcat gaagtacatc cagcatacgt acaggaaagg cgtcaagatt gacaagactg 480  
actacatggt aggcagctat gggccccggg ccgaggagta cgagttcctg acccccgtgg 540  
aggaggcacc caagggtatg ctggccccgg gcagctacag catcaagtcc cgcttcacag 600  
acgacgacaa gaccgaccac ctgtcctggg agtggaaatc caccatcaag aaggactgga 660  
aggactgagc ccagccagag gcgggcaggg cagagtgatg gacggaagac ggacaggcgg 720  
atgtgtcccc ccagcccct cccctcccca taccaagggtg ctgagcaggc cctccgtgcc 780  
cctccaccct ggtccgctc cctggcctgg ctcaaccgag tgctccgac cccctctctc 840  
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ccctcgatgg acaggcctga cccacccac ctggggccag ccaggagccc cgcctggggc 1560  
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accaagtga cacattgctg agagccgtct cctataggtc ccccgcccca tccccgtgt 1740  
tggtgtgtg tctgccagc tcaggcagag gcgcctgtcc ctgcttcttt tctgaccggg 1800  
aaataaatgc ccctgaagg 1819

&lt;210&gt; 412

&lt;211&gt; 306

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

259/292

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(306)

<223> 3' terminal sequence. complement component  
4a (C4A) gene.

&lt;400&gt; 412

```
gctgcacaaa gcctttaata tgccctggtc ccaggctgt g ttcattgaaag cggacacagc 60
agtgtttcca gtttcatggg tcccagggtt aggttcctcc cagcggagggt gggagggcag 120
ccctcacacc tggcaccctt gattgcatac tcctggagga agtcgttgag ctgggcacag 180
gtgcccgtt ggcgggttgcn tccggcacag gcgttcagag ggcatctcct cgatccagct 240
attcaggtcc agcaagta ct ngggggggnc cctcccaggg gcataantng gncntccag 300
anccat 306
```

&lt;210&gt; 413

&lt;211&gt; 5417

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(5417)

&lt;223&gt; complement component 4a (C4A) gene.

&lt;400&gt; 413

```
agaaggtagc agacagacag acggatctaa cctctcttgg atcctccagc catgaggctg 60
ctctgggggc tgatctgggc atccagcttc ttcaccttat ctctgcagaa gccaggttg 120
ctctgtttct ctcttctgtt ggttcatctg ggg gtcccc tatcgggtggg ggtgcagctc 180
caggatgtgc cccgaggaca ggtagtgaag ggatcagtg ttcctgagaaa cccatctcgt 240
aataatgtcc cctgctcccc aaaggtggac ttcacctta gctcagaaa agacttcgca 300
ctcctcagtc tccaggtgcc cttgaaagat gcgaagagct gtggcctcca tcaactcctc 360
agaggccctg aggtccagct ggtggcccat tcgccatggc taaaggactc tctgtccaga 420
acgacaaaac tccagggtat caacctgctc ttctcctctc gccgggggca cctctttttg 480
cagacggacc agcccattta caacctggc cagcgggttc ggtaccgggt ctttgctctg 540
gatcagaaga tgcgccgag cactgacacc atcacagtca tgggtggaga ctc tcacggc 600
ctccgcgtgc ggaagaagga ggtgtacatg ccctcgtcca tcttccagga tgactttgtg 660
atcccagaca tctcagagcc agggacctgg aagatctcag cccgattctc agatggcctg 720
gaatccaaca gcagcaccga gtttgagggt aagaaatatg tccttcccaa ctttgagggtg 780
aagatcaccc ctggaagacc ctacatcctg a cggtgccag gccatcttga tgaaatgcag 840
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tttggtctcc tagatgagga tggtaagaag actttcttcc gggggctgga gagtcagacc 960
aagctggtga atggacagag ccacatttcc ctctcaaagg cagagttcca ggacgcctg 1020
gagaagctga atatgggcat tactgacctc caggggctgc gcctctacgt tgctgcagcc 1080
atcattgagt ctccagggtg ggagatggag gaggcagagc tcacatcctg gtattttgtg 1140
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ttcctgctgc aggccttggg ccgtgagatg tcaggctccc cagcttct gg cattcctgtc 1260
aaagtttctt ccacgggtgc ttctcctggg tctgttcttg aagcccagga cattcagcaa 1320
aacacagacg ggagcgccca agtcagcatt ccaataatta tccctcagac catctcagag 1380
ctgcagctct cagtatctgc aggtctccca catccagcga tagccaggct cactgtggca 1440
gccccacctt caggaggccc cg ggtttctg tctattgagc ggccggatc tcgacctcct 1500
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cattactact acatgatcct atcccagggg cagatcgtgt tcatgaatcg agagcccaag 1620
aggacctga cctcgggtct ggtgtttgtg gaccatcacc tggcaccctc cttctacttt 1 680
gtggccttct actaccatgg agaccacca gtggccaact ccctgcgagt ggatgtccag 1740
gctggggcct gcgagggcaa gctggagctc agcgtggacg gtgccaagca gtaccggaac 1800
```

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ggggagtccg tgaagctcca cttagaaacc gactccctag ccctggtggc gctgggagcc 1860  
ttggacacag ctctgtatgc tgcaggcagc aagtc caca agcccctcaa catgggcaag 1920  
gtctttgaag ctatgaacag ctatgacctc ggctgtggtc ctgggggtgg ggacagtgcc 1980  
cttcagggtg tccaggcagc gggcctggcc ttttctgatg gagaccagtg gaccttatcc 2040  
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caaaaggcga ttaatgagaa attgggtcag tatgcttccc cgacagccaa gcgctgctgc 2160  
caggatgggg tgacacgtct gcccatgatg cgttcctgcy agcagcgggc agcccgcgtg 2220  
cagcagccgg actgccggga gcccttccctg tcctgctgcc aatttgctga gagtctgcgc 2280  
aagaagagca gggacaaggc ccaggcgggc ctccaacgag ccctggagat cctgcaggag 2340  
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gatccattgg acacttttag gctgtagggt gccttgtcac caggaggcgt ggcctccctc 3060  
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gcttcccgct acctggacaa gacagagcag tggagcacac tgcctcccga gaccaaggac 3180  
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aaggcgctg tggacctgct cggtgttgcc cacaacaacc tcatggcaat ggcccaggag 3720  
actggagata acctgtactg gggctcagtc actggttctc agagcaatgc cgtgtcgccc 3780  
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gacacggtag ttgcctgga tgccctgtct gcctactgga ttgcctcca caccactgag 4020  
gagaggggtc tcaatgtgac tctcagctcc acaggccgga atgggttcaa gtcccacgcg 4080  
ctgcagctga acaaccgcca gattcgcggc ctggaggagg agctgcagtt ttccttgggc 4140  
agcaagatca atgtgaaggt gggaggaaac agcaaaaggaa ccctgaaggt ccttcgtacc 4200  
tacaatgtcc tggacatgaa gaacacgacc tgccaggacc tacagataga agtgacagc 4260  
aaaggccacg tcga gtacac gatggaagca aacaggagact atgagtacga tgagcttcca 4320  
gccaaaggatg acccagatgc ccctctgcag ccgctgacac ccctgcagct gtttgagggt 4380  
cggaggaacc gccgcaggag ggaggcgccc aagggtggtg aggagcagga gtccagggtg 4440  
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atcacccaag tctgcactt caccaaggat gtcaaggccg ctgctaata gatgcgcaac 5040  
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aaagtgtcag tgttggc 5417

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<210> 414  
<211> 408  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(408)  
<223> 3' terminal sequence. cd3g antigen, gamma  
polypeptide (tit3 complex) (CD3G) gene.

<400> 414  
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tatttgagaa acccccaaatt ttgctctgat ggcctttctt ctccatttgt catctctggg 120  
aaccttgagt ctagatttag ggctgaaagt ctctctgcta ggagctttcc aaaatgcatt 180  
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ggggctggtg gagctggtca ttgggcaac a gagtctgctt gtctgnaagc tctcgactgg 360  
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<210> 415  
<211> 457  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(457)  
<223> 5' terminal sequence. cd3g antigen, gamma  
polypeptide (tit3 complex) (CD3G) gene.

<400> 415  
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aagatgacca gtacagccac cttcaagggn aaccagt 457

<210> 416  
<211> 822  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature

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&lt;222&gt; (1)..(822)

&lt;223&gt; cd3g antigen, gamma polypeptide (tit3 complex) (CD3G) gene.

&lt;400&gt; 416

```

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&lt;210&gt; 417

&lt;211&gt; 439

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(439)

<223> 3' terminal sequence. v-rel avian  
reticuloendotheliosis viral oncogene homolog b  
(nuclear factor of kappa light polypeptide gene  
enhancer in b-cells 3) (RELB) gene.

&lt;400&gt; 417

```

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gccgccccca aaggccgct 43 9

```

&lt;210&gt; 418

&lt;211&gt; 234

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(234)

<223> 5' terminal sequence. v-rel avian  
reticuloendotheliosis viral oncogene homolog b

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(nuclear factor of kappa light polypeptide gene  
enhancer in b-cells 3) (RELB) gene.

&lt;400&gt; 418

```
acgggggatg cccaacgtcc ttggggagct gaacagtctg gacccccatg gcatcgagag 60
caaacggcgg aagaaaaagc cggccatcct ggaccacttc ctgcccaccc acggctcagg 120
ccggttcctc ccgccgtcag cctgctgcc agaccctgac ttcttctctg ggcaccgtgt 180
tccctgcccg gcngggaggc cctggggggc ctgnacctcc tgggacgatg gggt      234
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&lt;210&gt; 419

&lt;211&gt; 2314

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2314)

<223> v-rel avian reticuloendotheliosis viral  
oncogene homolog b (nuclear factor of kappa light  
polypeptide gene enhancer in b-cells 3) (RELB)  
gene.

&lt;400&gt; 419

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gtttttgagc ctcaaaaaaa aaaaaaggaa ttcc 2314

&lt;210&gt; 420

&lt;211&gt; 214

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(214)

<223> 3' terminal sequence. estrogen receptor 1  
(ESR1) gene.

&lt;400&gt; 420

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acaaagcaaa gctgcgacaa aaccgagtca catcagtaat agtatgcac ggcaaaagg 180  
catattaatc catcaaacac aatttgcat ttga 214

&lt;210&gt; 421

&lt;211&gt; 520

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(520)

<223> 5' terminal sequence. estrogen receptor 1  
(ESR1) gene.

&lt;400&gt; 421

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agcgtaatt atgctctgtt tccaactgca ttctcttcc aattgaa tta aagtgtggcc 120  
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cagtgtagag ctcttgtttt atgggaaaag gctcaaatgc 520

&lt;210&gt; 422

&lt;211&gt; 6450

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc feature

&lt;222&gt; (1)..(6450)

&lt;223&gt; estrogen receptor 1 (ESR1) gene.

&lt;400&gt; 422

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actgcacat tcccaagtta atccctgaa aacttactct caactggagc aaatgaactt 5760
tggtccaaa tatccatctt ttcagtagcg ttaattatgc tctgtttcca actgcatttc 5820
ctttccaatt gaattaaagt gtggcctcgt ttttagtcat ttaaaattgt tttctaagta 5880
attgctgcct ctatta tggc acttcaattt tgcactgtct tttgagattc aagaaaaatt 5940
tctattcatt tttttgcac caattgtgcc tgaactttta aaatatgtaa atgctgccat 6000
gttccaaacc catcgctcagt gtgtgtgttt agagctgtgc acctagaaa caacatactt 6060
gtcccatgag cagggtcctg agacacagac ccttttgcac tcacagagag gtcatt tgggtt 6120
atagagactt gaattaataa gtgacattat gccagtttct gttctctcac aggtgataaa 6180
caatgctttt tgtgcactac atactcttca gtgtagagct cttgttttat gggaaaaggc 6240
tcaaatgcca aattgtgttt gatggattaa tatgcccttt tgccgatgca tactattact 6300
gatgtgactc ggttttgtcg cagctttgct ttgtttaatg aaacacactt gtaaacctct 6360
tttgcacttt gaaaaagaat ccagcgggat gctcgagcac ctgtaaacaa ttttctcaac 6420
ctatttgatg ttcaataaaa gaattaaact 6450

```

&lt;210&gt; 423

&lt;211&gt; 580

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(580)

<223> 3' terminal sequence. pre -b-cell leukemia  
transcription factor 1 (PBX1) gene.

&lt;400&gt; 423

```
ttaaacgtac aaacactttt attattttct ttgtaatttt tttcctcttt aaattcctct 60
aattgttgaa aatatccttc agtgatatgc gagagggcgg gcacccggga gtctaggaca 120
gaggcacagg ggcaggggaa atgacgaaaa ccaggctgac agctggaggc agggaagggt 180
ggcttctacc cagaaaaaaaa aggggagaga gtataaagaa gtgtccagat tggctgaaat 240
agcatcccaa agaagagaag agaaggagac tcttattgtg tttgc tgatt gcttcgacct 300
ccagtctgac cgcttcaggn ttgggagaga aaccctccct tcctgccct gccccaactg 360
ggcgacaggg tcagccggga tgcgattgct gggagatcag ttggaggtat cagagtgaac 420
actgccaggg ccttctgtag gggaggtcac tgatgaaggg gtagtagcat cctgcccaacc 480
tccattagca ctgatgccct gcg gactgta catctgactg gctgcgagtc catcactgta 540
tctcctgtc tggctgataa catggcgaag ggtatccacc 580
```

&lt;210&gt; 424

&lt;211&gt; 503

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(503)

<223> 5' terminal sequence. pre -b-cell leukemia  
transcription factor 1 (PBX1) gene.

&lt;400&gt; 424

```
gccaaagagg agttagccaa gaagtgtggc accacagtct cccagggtatc acaactgggt 60
tggaataaag cgaatccggt acaagaagaa cataggtaaa tttcaagagg aagccaatat 120
ttatgctgcc aaaacagctg tcactgctac caatgtgtca gcccatggaa gccaaagctaa 180
ctcgccctca actcccaact cggctggtgg atacccttcg ccatgttata agccagacag 240
gaggatacag tgatggactc gcagccagtc agatgtacag tccgcaggca tcagtgtctaa 300
tggaggttgg caggatgcta ctacccttc atcagtgacc t cccctacag aaggccctgg 360
cagtgttcac tctgatacct ccaactgac tccagcaat cgcattcccg ctgaccctgt 420
gccccagttg ggcaggggca ggagggaggg tttctctccc aacgctgaag cggtcagact 480
ggaggtcaaa cgattaggca aac 503
```

&lt;210&gt; 425

&lt;211&gt; 1819

&lt;212&gt; DNA/RNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1819)

<223> pre-b-cell leukemia transcription factor 1  
(PBX1) gene.

```

<400> 425
cttcctgtt tctcctgaaa aggatttgaa g acaagcttg aaggataaaa agccttggtg 60
cttcccagga gccgagccga ggagcagaag aggaagagcc gggggtgcc gtagcctttg 120
gagatggacg agcagcccag gctgatgcat tcccatgctg gggtcgggat ggccggacac 180
cccggcctgt cccagcactt gcaggatggg gccggaggga ccgaggggga gggcgggagg 240
aagcaggaca ttggagacat tttacagcaa attatgacca tcacagacca gagtttggat 300
gaggcgcagg ccagaaaaca tgctttaaac tgccacagaa tgaagcctgc cttgtttaat 360
gtgttgtgtg aaatcaaaga aaaaacagtt ttgagtatcc gaggagccca ggaggaggaa 420
cccacagacc cccagctgat gcggctggac aacatgctgt tagcggaaag cg tggcgggg 480
cctgagaagg gcggagggtc ggccgcagcg gcggcagcgg cggcggcttc tggaggggca 540
ggttcagaca actcagtga gcatcagat tacagagcca aactctcaca gatcagacaa 600
atctaccata cggagctgga gaaatacagc aggcctgca acgagttcac caccacgtg 660
atgaatctcc tgcgagagca aagccggacc aggccatct ccccaaagga gattgagcgg 720
atggtcagca tcatccaccg caagttcagc tccatccaga tgcagctcaa gcagagcacg 780
tgcgaggcgg tgatgatcct gcgttcccga tttctggatg cgcggcggaa gagacggaat 840
ttcaacaagc aagcgacaga aatcctgaat gaatatttct attcccatct cagcaaccct 900
taccacagtg aggaagccaa agaggagtta gccaaagaat gtggcatcac agtctcccag 960
gtatcaaact ggtttggaaa taagcgaatc cgttacaaga agaactatag taaatttcaa 1020
gaggaagcca atatttatgc tgccaaaaca gctgtcactg ctaccaatgt gtcagcccat 1080
ggaagccaa ctaactcgcc ctcaactccc aactcggctg gttcttcca g ttttttaac 1140
atgtcaaact ctggagattt gttcatgagc gtgcagtcac tcaatgggga ttcttaccaa 1200
ggggcccagg ttggagccaa cgtgcaatca cagggtgata cccttcgcca tggtatcagc 1260
cagacaggag gatacagtga tggactcgca gccagtcaga tgtacagtc gcagggcatc 1320
agtgtaatg gaggttgga gga tgctact accccttcat cagtgaacct ccctacagaa 1380
ggccctgga gtgttctc tgcatactcc aactgatctc ccagcaatcg catcccggct 1440
gaccctctgc cccagttggg gcaggggcag gagggagggt ttctctccca agctgaagcg 1500
gtcagactgg aggtcgaagc aatcagcaaa cacaataaga gtctcttct cttctcttct 15 60
ttgggatgct atttcagcca atctggacac ttctttatac tctcttccct tttttttctg 1620
ggtagaagcc acccttccct gcctccagct gtcagcctgg ttttgtcat cttccctgcc 1680
cctgtgcctc tgctcctagc ttcccggggt ccccgccctc tctcatatca ctgaaggata 1740
ttttcaacaa ttagaggaat ttaaagagga aaaaaat tac aaagaaaata ataaaagtg 1800
ttgtacgttt tcaaaaaaa 1819

```

<210> 426

<211> 506

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(506)

<223> 3' terminal sequence. gli-kruppel family

member gli3 (greig cephalopolysyndactyly syndrome)

(GLI3) gene.

<400> 426

```

taaaaagagg gtggtttgag tgtaacaata ctgattcaaa actgaaatgg aagacagttt 60
ctccctagaa tactttaggg tttttcagag tccttttcca taaa aggaat ataattgaaa 120
cacatctcag ttaggtgaga tgagattgct aaaatacata cagaactaaa aaaacagcca 180
aaacaaagtc agtttaatct cttcaactcc taatgatttc cggttggttc agtctttttt 240
tctaaagcc tattgcataa ctgcaaggga attgctttct tccgctaggg aggtcagcaa 300
agaactcatg tccccgatag cc atgttggt ggtgctcatg gacagcgtg ggaatgggag 360
ggacgcccga gggctgggta aagccgggaag aaactatgga aaagggtctca atgatacttg 420
ggctcagggc cccgacatca ggctcgagtg gtcccatct ctatgattgc atcgaagtca 480
atctggtacc ctcccaggcc aggctg 506

```

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<210> 427  
<211> 239  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(239)  
<223> 5' terminal sequence. gli -kruppel family  
member gli3 (greig cephalopolysyndactyly syndr ome)  
(GLI3) gene.

<400> 427  
ggcagaagga tcacttgagg ccaggcattc aagaccagcc tatgcaagat aatgagacct 60  
tgtctctatt taaaaaaciaa aaagcctggt gtggtggtgc atgcctgtag tctcagcctc 120  
ctgagtagct gggactataa gcacgcacca ctatgtctgg ctaatttttg tatttttagt 180  
agagacaggg tttcaccacg ttgccacggg cagtcttgaa ctctgacct caagtgatc 239

<210> 428  
<211> 5054  
<212> DNA/RNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(5054)  
<223> gli-kruppel family member gli3 (greig  
cephalopolysyndactyly syndrome) (GLI3) gene.

<400> 428  
cgatactacg tgggcatttt tggctgaaga gagctgaagt aatgagaaga catcatggag 60  
gcccagtcac acagctccac gaccactgaa aagaaaaaag ttgagaattc catagtgaag 120  
tgctccactc gaacagatgt gagcgagaaa gccgttgccct ccagcaccac ttctaagag 180  
gatgaaagtc ctggacagac ttatcacaga gagagaagaa acgcaatcac tatgcagcca 240  
cagaatgtcc aggggctcag caaagtcagt gaggaacctt caacatcgag tgacgagagg 300  
gcctcattga tcaagaaaga gatccatggg tccttgccac acgtggcgga gccctctgtg 360  
ccgtaccgag ggacgggtt tt tgccatggac ccaggaatg gttacatgga gcccactac 420  
caccctctc atcttttccc tgccttccat cctcctgtac caattgatgc cagacatcat 480  
gagggccggt accattacga tccatctcog attcctc  
cat tgcatatgac ttccgcctta 540  
tctagtagcc ctacgtatcc ggacctgcc ttcattagga tctcccaca ccggaacc cc 600  
gctgctgctt ccgagtctcc ctccagccct ccacatccct acattaatcc ctacatggac 660  
tatatccgct ccttgacag cagcccatcg ctctccatga tctcagcaac ccgtgggctg 720  
agccctacag atgcgcccc tgcaggagtc agccagcag aatactatca tcagatggcc 780  
ctgctaactg gccagcgag ccctatgca gacatt attc cctcagctgc caccgccggc 840  
acgggggcca tccacatgga atatcttcat gctatggata gcaccagatt ctccagcccc 900  
aggctgtcag ccaggccgag ccgaaaacgt aactgtcca taccacct ctccgatcat 960  
agctttgacc ttcagacat gataaggagc tctcccaact ccttggtcac gattctcaat 1020  
aattcccgta gca gctcttc agcaagtggc tcctatggtc acttatctgc aagtgaatc 1080  
agccctgect tgagcttcac ctactcttcc ggcggcgtct ctctccacat gcacgagcag 1140  
atcctaagcc gacaacagag cttaggttca gcctttggac acagccctcc actcatccac 1200  
cctgccccaa cttttccaac acagaggcct attccaggga tccctacggt tc tgaacccc 1260

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gtccagggtca gctccggccc ttctgagtc tccagaaca agccacagag tgagtctgca 1320  
 gtgagcagca ctgggtgacc gatgcacaac aagagggtcca agatcaaacc cgatgaagac 1380  
 ctccccagcc caggggctcg ggggcagcag gaacagcccg aaggaacaac ccttgtcaag 1440  
 gaggaagggg acaaatgatga aagcaaa cag gagcctgaag tcatctatga gacaaactgc 1500  
 cactgggaag gctgcgcgag ggagttcgac acccaagagc agcttgtgca ccatataaat 1560  
 aacgaccata ttcattggaga gaagaaggag ttctgtgtgca ggtggctgga ctgctcaaga 1620  
 gagcagaaac ccttcaaaag ccagtatatg ttggtagtgc atatgagaag acacacgggc 1680  
 gagaagcctc acaaatgcac ttttgaaggt tgacaaaagg cctactcgag actagaaaac 1740  
 ttgaaaacac acttgagatc tcacactgga gagaaccat acgtctgtga gcacgaaggt 1800  
 tgcaacaagg ctttctcaaa tgcctctgat cgcgcaaac accaaaacag aacgcattcc 1860  
 aatgagaac catatgtgtg caaaatccca gctgcacta agcgttacac agaccaagc 1920  
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 cgaggggaca tccctcctcg gccgcaacc cagagagatt ccggcagcca ttcacagtcc 2040  
 aggtcgccctg gccgacagcc tcaggagacc agcaggacct cagcaacact 2100  
 acctcaaacg gggaa gaatg cctccagggtg aaaaccgtca aggcagagaa gccaatgaca 2160  
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 gcggtctctc ctctcatagg aaatggcaca cagtccaaca acacctgcag cttgggtggg 2520  
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 atgctcaaca gaaggagcag cagcgcagc accatcagct cggcctacct gagcagccgc 2640  
 cgctcctcag ggatctcgcc ctgctctctc agccgcgct ccagcgaggc gtcacaggcc 2700  
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 tcgcgcgct ccagcgaagc cagccagagc gacggcctgc ccagcctgct cagcctcacg 2820  
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 ggagccacg gctacggcg gcgccacctg cagccgcagc atgcgctggg ccacggcgtg 3060  
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 cagaaccaag cagggtacga gcagcacttc cccagcgcgc tcccggacga cagcaa agtg 3420  
 cccacagggc ccgttgactt tgacgcgcgc gggtgcccag acagccacgc tggccagcag 3480  
 ttccatgccc tcgagcagcc ctgcccagag ggcagcaaaa ccgacctgcc cattcagtgg 3540  
 aacgaagtca gctccggaag cgcgcacctg tctctctcca agtcaagtg tgggcgcgcg 3600  
 cccgctgtgc cgcagactcg cgcctttggg ttctgcaacg gcatggtcgt ccaccgcag 3660  
 aaccccttga ggagcggggc tgctgggggc tatcagacc tcggggagaa cagcaacccc 3720  
 tacggtggcc cagagcactt gatgctccac aacagccccg gaagtggcac cagtggaaac 3780  
 gccttccatg aacagccctg taaggccccg cagtatggga actgtctcaa caggcagcca 3840  
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 gagtcagctg gcagcatggt gaatggcatg cagaaccagg acccagtggg acaggggtag 4020  
 ctggctcacc agctcctcgg cgacagcatg cagcaccgg gggc aggcgc ccccggtcag 4080  
 cagatgcttg ggcagattag tgctacctca cacatcaaca tctaccaagg gccagagagc 4140  
 tgcctgccag gggctcacgg catgggcagc cagccgtcaa gcttggcagt tgtcaggggc 4200  
 taccagccat gtgccagctt tgggggcagc aggcgcaggt ctatgccgag ggacagcctt 4260  
 gctctcgagt caggacagc t cagtgcacaa agtcagacct gcagggtgaa tggatatcaag 4320  
 atggagatga aagggcagcc ccatccgctg tgctctaatc tgcagaatta ctctggtcag 4380  
 tttctatgacc aaaccgtggg cttcagtcag caagcacgaa aagctgggtt attctctatt 4440  
 tcagacgcca gctgcctgct acaggggacc agcgccaaa actctgagtt actttccc ca 4500  
 ggtgctaate aggtgacaag cacagtggac agcctcgaca gccatgacct ggaaggggta 4560  
 cagattgact tcgatgccat catagacgat ggggaccact ccagcctgat gtcggggggc 4620  
 ctgagcccaa gtatcattca gaacctttcc catagctcct cccgcctcac cagcctcgg 4680  
 gcgtccctcc cattcccagc gctgtccatg ag caccacca acatggctat cggggacatg 4740  
 agttctttgc tgacctccct agcgggaagaa agcaaatcc ttgcagttat gcaataggct 4800  
 tttagaaaaa aagactgcaa ccaacggaaa tcaataggag ttgaagagat taaactgact 4860  
 ttgttttggc tgttttttta gttctgtatg tatttttagca atctcatctc acctaaactga 4920

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gatgtgtttc aattatattc cttttatgga aaaggactct gaaaaaccct aaagtattct 4980  
aggagagaaac tgtcttccat ttcagttttg aatcagtatt gttacactca aaccaccctc 5040  
tttttaaaaa aaaa 5054

<210> 429  
<211> 271  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(271)  
<223> 3' terminal sequence. interleukin enhancer  
binding factor 1 (ILF1) gene.

<400> 429  
aggagacttg ttttactcag agtggaaaat ttggccaggg acaaagtc aa cacaaagaaa 60  
caaacaacaa aaaatagcca gaaagagaaac agttaagtgc agctcgggtga gtcccggcag 120  
ttccttcccg gcactggctc gtccctgggt tctcaagggt ccatgcggcc acagcgtccg 180  
tccacctgct cagcgagcc acatgctgaa atggaggtgg ataaaattca tcaggcagct 240  
gctgtaacac ggaaatgtgc agatgcc aga g 271

<210> 430  
<211> 193  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(193)  
<223> 5' terminal sequence. Similar to Retinoblastoma -like protein 2,  
sw|Q08999|RBL2\_HUMAN.

<400> 430  
TGTCTACATT TNCCCACATA AAAATGAAAC AATNNTTCT CCTCGNGAAA AGATTTTATA 60  
TTRACTTNAGC NAAAGTCCTT CAAAGNGACT GAGCGNANNT AATAGTNTGA TACGCATAGG 120  
NGNAACTCCT ACTNNAANGN GCGGNNTTCT TNTNGNNGAT GGCNGTGAAT NCACTGCAAA 180  
NAGCATTTGC CCN 193

<210> 431  
<211> 184  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(184)  
<223> 3' terminal sequence. Homo sapiens CD2 antigen (p50).



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&lt;400&gt; 431

AGTCAAAGCT TTTATTTCAC TTTNACTCAC AGGATGGGGG GCAAGTNTCC ACCAGGGCAC 60  
ATAAGAACT CCAGAGTCTC TTAAGCAGAT AGGCTGCTTG TAGNGAGACC CAGGNACACC 120  
AATCACTGA TTTATCGCAT CTACACATGA CCNGAGAGGG GACAAGAAAT CTCTAAGTTT 180  
TCTG 184

&lt;210&gt; 432

&lt;211&gt; 242

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(242)

&lt;223&gt; 5' terminal sequence. Similar to NM\_022641 Homo sapiens chorionic somatomammotropin hormone 1 (placental lactogen) (CSH1

&lt;400&gt; 432

ATTCGGCACG ATGACTGGCC AGGGTATAAA AAGGGCCCAC AAGAGACCGG CTCTAGGATC 60  
CCAAGGCCCA ACTCCCCGAA CCACTCAGGG TCCTGTGGCA GCTCACCTAG TGGCAATGGC 120  
TCCAGGCTCC CGGAACGTCC CTGATCCTGG NTTTTGNCCT NCTCTNACTG CCCTGGNTTN 180  
AANAAGCTNG TGCCNTCCAA ANCGTCCGT TATCCAGGGT TTTTGACCAC GCTATGCTNC 240  
AA 242

&lt;210&gt; 433

&lt;211&gt; 329

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(329)

&lt;223&gt; 5' terminal sequence. Homo sapiens plasminogen activator (PLAT)

&lt;400&gt; 433

AACAGTCACC GACAACATGC TGTGTGCTGG AGACACTCGG AGCGGCGGGC CCCAGGNAAA 60  
CTTGACGAC GCCTGCCAGG GNATTTCGGG AGGCCCCCTG GTGTGTCTGA ACGATGGCCG 120  
CATGACTTTG GTGGGCATCA TCAGCTGGGG CCTGGGCTNT GGACAGAAGG ATGTCCCGGG 180  
TGTGTACACC AAGGTTACCA ACTACCTAGA CTGGATTTCGT GACAACATGC GACCGTGACC 240  
AGGAACACCC GACTCCTCAA AAGNAAATGA GATCCCGNCT CTTCTTCTTC AG AAGACACT 300  
GCAAAGGCGC AGTGCTTCTC TACAGACTT 329

&lt;210&gt; 434

&lt;211&gt; 247

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

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&lt;222&gt; (1)..(247)

&lt;223&gt; 3' terminal sequence. Homo sapiens plasminogen activator (PLAT)

&lt;400&gt; 434

AAATATATCT GAANNNTTA AGTACAGTNT AAAACAGGGT TNTGGCAACA GAAAGTAAAA 60  
ACTAACATGG NTTGCTATAA ATATGCTGAA GCCTAGTTGT TCAAATGATA CAATTCTCTC 120  
ATGCTACTCT AAAGTTTNTA AAGNAAAAGG GTTTACACTT TACACACT GT ACACAAAGGG 180  
GNTACCTTCT GNGNGCCNGG GAGTGGGGAA AGGGGANGGN GACTTGACGT CAAGGGTGCT 240  
TTTGAGG 247

&lt;210&gt; 435

&lt;211&gt; 63

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(63)

&lt;223&gt; 5' terminal sequence. Homo sapiens aminoacylase 1 (ACY1).

&lt;400&gt; 435

CCGCCAGNAC CTGCGTATCC GCACTGTTCA GCCCAAGCCT GACTATGGAG CTGCTGTGGC 60  
TTT 63

&lt;210&gt; 436

&lt;211&gt; 190

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(190)

&lt;223&gt; 3' terminal sequence. Homo sapiens aminoacylase 1 (ACY1).

&lt;400&gt; 436

GAAGAGGAGG NCCTTGGCAC TGGTNGGGAN GGAAGCCCCA GGGGAAAAGG TTNAGGAGTC 60  
CCAGGGCTCA GCTGTCACTG GGCAGGGCAG GCACACTGGC AGGGCCAGGC AGCAGGCNNG 120  
TATATATGNC CACCCACGG AGGAACACAG CCTNATGCAG NCGTTNATCG TGGTNGTGCA 180  
GNAGCACAGG 190

&lt;210&gt; 437

&lt;211&gt; 176

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(176)

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<223> 3' terminal sequence. Homo sapiens E74 -like factor 1 (ets domain transcription factor) (ELF1)

<400> 437

CCCTTAGGCT GTTCTGGTGA TGAGGCTCCC GGTGAGTCTG CATATTTTNN TTGCACCTGC 60  
TGTGTTTCCA TCACTTCAGG AATCCCATCT AATGTGACGG ACACATGGGT GACTGGGGCA 120  
ACAACCATGT CATCTTCAGG NGAACATAAT ATATTATTAT TTATCCGGTT TTCATC 176

<210> 438

<211> 465

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(465)

<223> 5' terminal sequence. Homo sapiens selectin P,  
granule membrane protein CD62, SELP

<400> 438

NGGAACATAT GGAGTTTTTA CA AACGCTGC ATTTGACCCG AGTCCTTAAG AGACCTGTCC 60  
TTTTCTGGT CTCCTCATTC AGCCTCCATA TGATCCTGTT GTGAACATCA AGTTTCCTGC 120  
TACACTGGAC TTAACATATAA TGCACTTGCT GCAGGTTTCC ATAAACACCC ATGANTCAAA 180  
GACATGGAAT TACCTTAGAT TAGCTCTGGA CCAGCCTGTT GGACCCGCTC TGGACCAACC 240  
CTGTTTCCCTG AGTTTGGGAT TGTGGTACAA TCTCAAATTC TCAACCTACC ACCCCTTCCT 300  
GTCCACCTC TTCTCTTCCT GTAACACAAG CCACAGAAGC CAGGAGCAAA TGTTTCTGCA 360  
GTAGTCTCTG TGCTTTGACT CACCTGTTAC TTGAAATACC AGTGAACCAA AGAGACTGGA 420  
GCATCTGGAC TTNACAAGAA GACCAGACTT GTGGAGANAT TAA AA 465

<210> 439

<211> 396

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<220>

<221> misc\_feature

<222> (1)..(396)

<223> 3' terminal sequence. Homo sapiens selectin P,  
granule membrane protein CD62, SELP

<400> 439

GAAAATCCTT TNAATTACGN ATTTNAANAT TGGNCTTTGG GNCATTTGAG GGACAGTGAC 60  
TGGGGGCAGG AAGGCCCCAG GNGACATGTG GCCTTCTAGC TTNATNCTTG GCCTTCTGCA 120  
GCCTCTGGGG CCATCCAGAG GACTCTCTGG AAGCCTCAGA GCAGAGGNCC AAGAGGCCCTC 180  
ATCAACAGCA ACCANTGGAG ACTCCAGAAG ATGCTACAGG ANTTNCTCCC AATTAGAGAT 240  
GCCACCTGTT TNCCAACAAA GTGGAGAAAA CCTTCCTNNA ATCAAAAANT AAAGAGGTNT 300  
TTCNATTTCT CCACAGTTTG GCCTCCTTGT GAGTCAGATG NTCCAGTCTC TTTGGNNCAC 360  
TGGTATTTC AATAACAGGT GAGNNAAGG ANAGAG 39 6

<210> 440

<211> 337

<212> DNA

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&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(337)

&lt;223&gt; 5' terminal sequence. Human interleukin 3 receptor (hIL -3Ra).

&lt;400&gt; 440

```
AAAGGCTCAG CAGTTGAC CT GGGACCTTAA CAGAAATGTG ACCGATATCG AGTGTGTTAA 60
AGACGCCGAC TATTCTATGC CGGCAGTGAA CAATAGCTAT TGCCAGTTTG GAGCAATTTC 120
CTTATGTGAA GTGACCAACT ACACCGTCCG AGTGGCCAAC CCCCATTCT CCACGTGGAT 180
CCTCTTCCCT GAGAACAGTG GGAAGCCTTT GGCAGGTGCG GAGAATCTGA CCTGCTNGAT 240
TCATGACGTT GATTTCTTGA GCTGCAGCTG GCGGGTAGGG CNCGGGGCC CGCGGGACGT 300
CCAGTACGAC CTGTACTTGA ACGTTNCCAA CAGGNGT 337
```

&lt;210&gt; 441

&lt;211&gt; 104

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:prim er

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(104)

&lt;223&gt; 3' terminal sequence. Human interleukin 3 receptor (hIL -3Ra).

&lt;400&gt; 441

```
TTCCCCCTC CCAGACCACC AGNTTGNCGT TTTGGNAGNT NTNACCGANG GGGTNTTNCA 60
TGTNAGGGNT NCGGGNAAAN AGTTTNTGAA NCACCAGAAA CCTT 104
```

&lt;210&gt; 442

&lt;211&gt; 223

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(223)

&lt;223&gt; 5' terminal sequence. Human tumor protein p53 (Li -Fraumeni syndrome) (TP53)

&lt;400&gt; 442

```
AAGCAATGGA TGATTTGATG CTGTCCCCGG ACGATATTGA ACAATGGTTC ACTGAAGACC 60
CAGGTCCAGA TGAAGCTCCC AGAATGCCAG AGNTGNCTCC CCGCGTGGCC CCTGCACCAG 120
CAGCTCCTAC ACCGGCNGCC CCTGCACCAG CCCCTCCTG GCCCTGTCA TCTTCTGTCC 180
CTTCCAGAN AACCTACCAG GGCAGCTACG GTTCCGTCT G GG 223
```

&lt;210&gt; 443

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<211> 223  
<212> ADN  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(223)  
<223> 5' terminal sequence. Tumor protein p53  
(Li-Fraumeni syndrome) (TP53) gene.

<400> 443  
aagcaatgga tgatttgatg ctgtccccgg acgatattga acaatgggtc actgaagacc 60  
caggtccaga tgaagctccc agaatgccag agntgnctcc ccgcgtggcc cctgcaccag 120  
cagctcctac accggcngcc cctgcaccag cccctcctg gccctgtca tcttctgtcc 180  
cttcccagan aacctaccag ggcagctacg gtttccgtct ggg

<210> 444  
<211> 343  
<212> ADN  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(343)  
<223> 3' terminal sequence.

<220>  
<221> misc\_feature  
<222> (1)..(343)  
<223> v-erb-b2 avian erythroblastic leukemia viral  
oncogene homolog 2 (neuro/glioblastoma derived  
oncogene homolog) (ERBB2) gene.

<400> 444  
caaggggctg caaactnncc cacacatgac cccagccctc tacagcggtg cagtgaggac 60  
cccacagtac ccctgccctc tgagactgat ggctacgttg cccccctgac ctgcagcccc 120  
cagcctgaat atgtgaacca gccagatgtt cgccccagc ccccttcgcc ccgagaggcc 180  
ctctgcctgc tgcccgacct gctggtgcca ctctggaaag gcccaagact ctctccccag 240  
ggaagaatgg ggtcgtaaaa gagtttttgc cttt gggggt gccgtgggag aaccccgagt 300  
attgacaccc caggggaggg agcttgccct tcagccccac ctt 343

<210> 445  
<211> 309  
<212> ADN  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(309)  
<223> 3' terminal séquence.

<220>  
<221> misc\_feature  
<222> (1)..(309)  
<223> zinc finger protein 144 (Mel -18) (ZNF144) gene.

<400> 445  
ccgcccccca cccccaaggt gganagagct ggggaaagta gaagaggtgg aaaaaagggc 60  
ccagaaaaag tggaaggagt ggagaggctt ag ctggaaga agggagaggg tccctggcct 120  
caagttaagg ggggcacggg agcgccnttg acagtcattt tgcgccccct gctggtngaa 180  
ganggtttct tcaggcagtt caagctaccc ccgttngcan ctttngnngc cccacttgct 240  
ntcgaagggg ganttgggna ngtagggtn gtnngcttgan gcccatngga actnggaaaa 300  
ccatnggat 309

<210> 446  
<211> 268  
<212> ADN  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(268)  
<223> 3' terminal sequence.

<220>  
<221> misc\_feature  
<222> (1)..(268)  
<223> MAP/microtubule affinity-regulating kinase 3  
(MARK3) gene.

<400> 446  
attatcttgt gaatctactt agaaaaacac acacaagcaa tgttcacaac tataaattta 60  
aaccttttgc actaaaaaaa cacaaaaaca caaacacaan accacaggca tgaactgtaa 120  
acctgtatta actntgaact ggtcttaagg ttaattctta gcngtcattc agtattttcc 180  
tccttggcaa ctgtaatgtt ttngcaccgg ntgatctccc gcnggggggta ctagtaatga 240  
ctggctgccc gtgtaggag atgcttcc 268

<210> 447  
<211> 169  
<212> ADN  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(169)  
<223> 5' terminal sequence.

<220>  
<221> misc\_feature  
<222> (1)..(169)  
<223> MAP/microtubule affinity-regulating kinase 3  
(MARK3) gene.

<400> 447

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gaacactgat ggaaatgtat agaataatat ttaggcaata acgtctgcat cttctaaatc 60  
atgaaattaa agtctgagga cgagagcacg nctggngcg aaantntgcc tttttntac 120  
ggatgcacta cantaaagan gtgcanccta tncgncccct gccctactt 169

<210> 448  
<211> 393  
<212> ADN  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(393)  
<223> 3' terminal sequence.

<220>  
<221> misc\_feature  
<222> (1)..(393)  
<223> EST N68536 MAX-interacting protein 1 (MXI1) gene.

<400> 448  
aagtaattaa gggtagttaa attattttaa gtatacaaag tccaaacagc caggggtaag 60  
gtctccaaga ggccttccca gggtaagga gagggccaca agggaacctt ggagtttgaa 120  
agacaaaggg aacacatgac atcaaagtgc aggctagaaa ttctacttag aagaaaataa 1 80  
cattactgaa aatattcgta agagtaacaa tagcacatgc acagtgggac tgtgaggaag 240  
agagagactg cctgtaggaa aatggaagca aatctttaca ttaaaatgag acaagtgcctg 300  
aacttactat gttaactatg atagtgtgtc tacnatagat atcncgatgg ttaaaagctg 360  
gtaaaagga atggttctca aaaccnaaa a tag 393

<210> 449  
<211> 217  
<212> ADN  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(217)  
<223> 5' terminal sequence.

<220>  
<221> misc\_feature  
<222> (1)..(217)  
<223> EST R81126 lymphotoxin beta receptor (LTBR) gene.

<400> 449  
ttacntgggt atctcctact gtagtatgag gaagaatggc tgtaaatgta ttttttgaat 60  
tctggnctca cctttgtctc agctaaatgt agccgcaccc gggacacagt ttgtgccaca 120  
tgtgccgaga attcctacaa cgagc actgg aactacctga ccatctgcca nctgtgccgc 180  
ccctgtgacc cagtgatggg cctcgnctga gantgcc 217

<210> 450  
<211> 157  
<212> ADN

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&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(157)

&lt;223&gt; 5' terminal sequence

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(157)

&lt;223&gt; (POU2F2) gene.

&lt;400&gt; 450

nattcggcaa cgnggaaagg aaagaaacta accaacaata gagaaaacca aaaataatca 60  
caacagaaac cagctgcccc aaaggaggcc agtngtnggg acgcagaggg tcc tcagagc 120  
aggagtnaca agggaggaaa gaccaaaaaa acaacca 157

&lt;210&gt; 451

&lt;211&gt; 282

&lt;212&gt; ADN

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(282)

&lt;223&gt; 5' terminal sequence.

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(282)

<223> caspase 4, apoptosis-related cysteine protease  
(CASP4) (ex CASP1)

&lt;400&gt; 451

gagaatctga cagccaggga tatggagtca gcgctgaggg catttgctac cagaccagag 60  
cacaagtcct ctgacagcac attcttggtg ctcattgtctc atggcctcct ggagggaatc 120  
tgcggaactg tgcattgatga gaaaaaacca gatgtgctgc tttatgacac catcttccag 180  
atattcaaca accgcaactt gcctcagtct ngaaggacaa acccaaggtc atcattgtnc 240  
agggtttgca gaggggtgcaa accttggggg aantttgggg tc 282

&lt;210&gt; 452

&lt;211&gt; 424

&lt;212&gt; ADN

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(424)

&lt;223&gt; 5' terminal sequence



<220>  
<221> misc\_feature  
<222> (1)..(424)  
<223> syndecan 1 (SDC1) (ex HRB)

<400> 452  
ttgcttttng caaaactota cttaatccaa tnggtttttc cctgtacagt agattttcca 60  
aatgtaataa actttaatat aaagtagtcc tgtgaatgcc actgccttcg cttcttgcc 120  
ctgtgctgtg tgtgacgtga ccggactttt ctgcaaacac caacatgttg ggaaacttgg 180  
ctcgaatctc tgtgccttcg tctttcccat ggggagggga ttctggttcc agggccctc 240  
tgtgtatttg cttttttgtt ttggtgaaa ttctcctgga ngtcggtagg ttcagccaag 300  
gttttataag ggctgatgtc aatttncgtg gtttgccaan ttccaagccc catcttncta 360  
aatgggcaaa aggaaggtgg gatgggcccc agcnacagct ttgnacc ga gggctnttgg 420  
gtca 424

<210> 453  
<211> 435  
<212> ADN  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(435)  
<223> 5' terminal sequence

<220>  
<221> misc\_feature  
<222> (1)..(435)  
<223> Integrin, beta 2 (antigen CD18 (p95), lymphocyte  
function-associated antigen 1; macrophage antigen  
1 (mac-1) beta subunit) (ITGB2)

<400> 453  
aggagtgcgc cggctgcccc tcacct gtg gcaagtacat ctctgcgcc gaggccctga 60  
agttcgaaaa gggccctnt ggaagaactg cagcgcgccg tgcggggcc tgcagctgtc 120  
gaacaacccc gtgaaggcca ggacctgcaa ggagaggac tcagagggt gctgggtggc 180  
ctacacgtg gagcagcagg acgggatgga ccgctacctc atctatgtg atgagagccg 240  
agagtgtgtg gcaggcccca acatcgccgc catcgctcgg ggcaccgtgg gcaggcatcg 300  
tgctgatcgg cattctctg ctggtcatct gggaaggctc tgatccacct gagcgacctc 360  
cgggagttac aggcgttttg agnaggagaa gctcaagtcc cagtnggaac aatgattatt 420  
ccctttttca agagc 435

<210> 454  
<211> 544  
<212> ADN  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(544)

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&lt;223&gt; 5' terminal sequence

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(544)

<223> Protein phosphatase 1, catalytic subunit, alpha  
isoform (PPP1CA) (ex MGST1)

&lt;400&gt; 454

```
gtgtgaccag acatgcaacc gncatctatg gtttctacgn atgnagtgn c aagcagnacg 60
nctnacaaca tcaaaactgtg gnaaaacctt cactgnactg ncttcaactg ncctgnccca 1 20
tcgcggncca tagtggaagt aaaagatctt ctgncctgncc acggaggcct gttccccgga 180
cctgncagtt ctatggnagc agattcggcg ggatcatgcg gccacacagat gtgtcctgta 240
ccaggggcct gctgtgtgac ctgctgtggt ctgaccctga caaggacgtg cagggctggg 300
gcgagaacga ccgtggcggt ctcttttac c tttggagccg aggtggtggc caagttcctc 360
cacaagcacg acttggaact catctgccga gcacaccagg ttgtagaaga cggctacgag 420
ttctttgccg agcggcantt ggtgacactt ttctcagctt ccaactactg ttgcgagttt 480
nacaatgctt gcgccatgat gagtgtgacg agaccctatg tgcttttcag atcttaagcc 54 0
gccn 544
```

&lt;210&gt; 455

&lt;211&gt; 344

&lt;212&gt; ADN

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(344)

&lt;223&gt; 3' terminal sequence

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(344)

<223> protein phosphatase 2 (formerly 2A), catalytic  
subunit, alpha isoform (PPP2CA)

&lt;400&gt; 455

```
actgcggtga gagccagcgg ccagcgccac cncaacagcc gccagaagna cagcaggaac 60
cggcggcggc gngtgcgngt aggcccggtg n gcggtgncgg cgcgggagga gccggannca 120
gccggcnggg gcgggnggca ncanggacga gaaggngnnc accaaggagc tggaccagn 180
gaacgagcag cngaacgagn gcaagcagcn gnccgagncc caggncaga gccncagcga 240
gaangcnaaa gaaanccnga caaaagaanc caacngcaa gaggnncgan gnccagnnac 30 0
ngnccgngga gangngcang ggcaannnca ngaacccatg gaac 344
```

&lt;210&gt; 456

&lt;211&gt; 514

&lt;212&gt; ADN

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(514)

&lt;223&gt; 5' terminal sequence

<220>  
<221> misc\_feature  
<222> (1)..(514)  
<223> S100 calcium-binding protein A11 (calgizzarin)  
(S100A11)

<400> 456  
cagcctcccg cgctcgctc agctccaaca tggcaaaaat ctccagccct acagagactg 60  
agcgggtgcat cgagtccttg attgctgtct tccagaagta tgctggaa ag gatgggtata 120  
actacactct ctccaagaca gagttcctaa gtttcatgaa tacagaacta gctgccttca 180  
caaagaacca gaaggaccct ggtgtccttg accgcatgat gaagaaactg gacaccaaca 240  
gtgatgggtca gctagatttc tcagaatttc ttaatctgat tgggtggccta gctatggctt 300  
gccatggact ccttcctcaa ggctgtccct tcccagaagc gggacctgga gggacccctt 360  
gggcccctggg cctttcaaac ccacccccctn ttcctttcca gcctttctgt tcatcatntt 420  
ccacagccca cccttncctg gaggcacatt aaccacctna tggtagggtg ccaactggtc 480  
attagttatt aaaggnaatg tnaatttttt ttaa 514

<210> 457  
<211> 359  
<212> ADN  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(359)  
<223> 5' terminal sequence

<220>  
<221> misc\_feature  
<222> (1)..(359)  
<223> Granzyme A (granzyme 1, cytotoxic  
T-lymphocyte-associated serine esterase 3) (GZMA)

<400> 457  
gctggacgtc atcaacaagc attcattcaa caacttccgc ctgcgagtgg ggttgaacca 60  
tggaccogta gtagctggag ttattggggc ccagaagccg caatatgaca ttgggggcaa 120  
cacagtgaac gtggccagcc gcatggagag tacaggagtc cttggcaaaa tccaagtgaac 180  
tgaggagaca gcatggggccc tacagtcctt gggctacacc tgctacagcc nggggtgtca 240  
tcanggtgaa aggcaaaggg cagctctgca cctacttcct gaacacagac ttgacacgaa 300  
ctggacctcc ttcagctacc ctaggctgag attgactcg cct tncctaag aacctnaat 359

<210> 458  
<211> 1251  
<212> ADN  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(1251)  
<223> 3' terminal sequence

<220>

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&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(1251)

&lt;223&gt; endothelin 1 (EDN1)

&lt;400&gt; 458

```
ggagctgttt accccactc taataggggt tcaatataaa aagccggcag agagctgtcc 60
aagtcagacg cgctctgca tctgcgccag gcgaacgggt cctgcgcctc ctgcagtccc 120
agctctccac caccgcgcg tgcgctgca gacgtccgc tcgctgcctt ctctcctggc 180
aggcgtgccc ttttctcccc gttaaagggc acttgggctg aaggatcgct ttgagatctg 240
aggaaccgcg agcgcttga gggacctgaa gctgttttcc ttcgttttcc tttgggttca 300
gtttgaacgg gaggtttttg atcccttttt ttcagaatgg attatttgct catgattttc 360
tctctgctgt ttgtggcttg ccaaggagct cc agaacag cagtcttagg cgctgagctc 420
agcgcggttg gtgagaacgg cggggagaaa cccactccca gtccaccctg gcggctccgc 480
cgggtccaagc gctgctcctg ctgcctcctg atggataaag agtgtgtcta cttctgccac 540
ctggacatca tttgggtcaa cactcccag cactgtgttc cgtatggact tggaaagccct 600
aggccaaga gagccttgga gaatttactt cccacaaagg caacagaccg tgagaataga 660
tgccaatgtg ctagccaaaa agacaagaag tgctggaatt tttgccaagc aggaaaagaa 720
ctcagggtcg aagacattat ggagaaagac tgggaataatc ataagaaagg aaaagactgt 780
tccaagcttg ggaanaagtg tatttatcag cag ttagtgga gaggaagaaa aatcagaaga 840
agttcagagg aacacctaag acaaaccagg tcggagacca tgagaacacg cgtcaaatca 900
tcttttcatg atcccaagct gaaaggcaag cctccagag agcggttatgt gaccacaac 960
cgagcacatt ggtgacagac ttcggggcct gtctgaagcc atagcctcca cggagagccc 1020
tgtggccgac tctgactct ccaccctggc tgggatcaga gcaggagcat cctctgctgg 1080
ttcctgactg gcaaaggacc agcgtcctcg ttcaaaacat tccaagaaag gttaaggagt 1140
tcccccaacc atcttactg gcttccatca gtggtaactg ctttgtctc ttctttcatc 1200
tggggatgac aatggacctc tcagcagaaa caca cagtca cattogaatt c 1251
```

&lt;210&gt; 459

&lt;211&gt; 2145

&lt;212&gt; ADN

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2145)

&lt;223&gt; 3' terminal séquence

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2145)

<223> Protein tyrosine phosphatase, non -receptor type 6  
(PTPN6)

&lt;400&gt; 459

```
cggcagaact gggaccaccg ggggtggtga ggcggcccgg cactgggagc tgcattctgag 60
gcttagtccc tgagctctct gcctgccag actagctgca cctcctcatt ccctgcgccc 120
ccttctctc cggaagcccc caggatgggt aggtggttcc accgagacct cagtgggctg 180
gatgcagaga ccctgctcaa gggccgaggt gtccacggta gcttcttggc tcggccagct 240
cgcaagaacc agggtgactt ctgcctctcc gtccaggggtg gggatcaggt gacctatatt 300
cgatccaga actcaggga tttctatgac ctgtatggag gggagaagt t tgcgactctg 360
acagagcttg tggagtacta cactcagcag cagggtgttg tgcaggaccg cgacggcacc 420
atcatccacc tcaagtaccc gctgaactgc tccgatccca ctagtgagag gtggtaccat 480
ggccacatgt ctggcgggca ggcagagacg ctgctgcagg ccaagggcga gccctggacg 540
tttcttgtgc gtgaga gcct cagccagcct ggagacttctg tgctttctgt gctcagtgc 600
cagcccaagg ctggcccagg ctccccgctc agggtcaccc acatcaaggt catgtgcgag 660
ggtggacgct acacagtggg tggtttgag accttcgaca gcctcacgga cctgggtggag 720
```

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```

catttcaaga agacggggat tgaggaggcc tcaggcgccct ttgtctacct gcggcagccg 780
tactatgcc a cgagggtgaa tgcggtgac attgagaacc gagtgttggg actgaacaag 840
aagcaggagt ccgaggatac agccaaggct ggcttctggg aggagtttga gagtttgag 900
aagcaggagg tgaagaactt gcaccagcgt ctggaagggc aacggccaga gaacaagggc 960
aagaaccgct acaagaa cat tctcccttt gaccacagcc gagtgatcct gcagggacgg 1020
gacagtaaca tccccgggtc cgactacatc aatgccaact acatcaagaa ccagctgcta 1080
ggccctgatg agaacgctaa gacctacatc gccagccagg gctgtctgga ggccacggtc 1140
aatgacttct ggcagatggc gtggcaggag aacagccgtg tcatcgatcat gaccaccga 1200
gaggtggaga aaggccggaa caaatgcgtc ccatactggc ccgaggtggg catgcagcgt 1260
gcttatggc cctactctgt gaccaactgc ggggagcatg acacaaccga atacaaactc 1320
cgtaccttac aggtctcccc gctggacaat ggagacctga ttcgggagat ctggcattac 1380
cagtacctga gctggccc ga ccatggggtc cccagtgagc ctgggggtgt cctcagcttc 1440
ctggaccaga tcaaccagcg gcaggaaagt ctgcctcacg caggggccat catcgtgcac 1500
tgccagccg gcacggcg cgacaggcacc atcattgtca tcgacatgct catggagaac 1560
atctccacca agggcctgga ctgtgacatt gacatccaga agaccatcca g atggtgcg 1620
gcgcagcgt cgggcatggt gcagacggag gcgcagtaca agttcatcta cgtggccatc 1680
gccagttca ttgaaaccac taagaagaag ctggaggtcc tgcagtcgca gaaggccag 1740
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tcccgcaact cgtccaaac a caaggaggat gtgtatgaga acctgcacac taagaacaag 1860
agggagaga aagtgaagaa gcagcgggtca gcagacaagg agaagagcaa gggttccctc 1920
aagaggaaat gagcgtgtgt gtcctcaggt ggccatgcct cagccctgac cctgtggaag 1980
catttcgca tggacagact cacaacctga acctaggagt gcccattct tt tgtaattt 2040
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cagggccaac ccttctctc ttgtaaataa agccctggga tcaact 2145

```

&lt;210&gt; 460

&lt;211&gt; 2149

&lt;212&gt; ADN

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2149)

&lt;223&gt; 3' terminal sequence

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(2149)

&lt;223&gt; Transcription factor AP-4 (activating enhancer binding protein 4) (TFAP4)

&lt;400&gt; 460

```

gacctgcaaa cacacacac a cacacacaca cacacacaca cacacacaca catacacacg 60
caccagggca gccgagagac ctccctcccg cccctcccat gccgcctcc ctccctcgc 120
cgccgcccgc gccgccagca tctgggaccg gccgattctg cacctccgtc cgccgctgcc 180
ctttgattcg gatttccatc ttgcattctc cggtgatcg cgggacctgg ct cgtgcaga 240
ggaggggggc cgatcgctat ggagtatttc atggtgccc ctcagaaggt gccctctttg 300
caacatttca ggaaaacaga gaaagaagt ataggagggc tctgtagcct tgccaacatt 360
ccactaacc ccgagactca gcgggaccag gcgcggcgga ttggcgggga gatcgccaac 420
agcaacgagc ggagacgcat gcagagcatc aacgcgggat tccagtccct caagaccctc 480
atccccaca cagacggaga gaagctcagc aaggcagcca ttctccagca gacagccgag 540
tacatcttct cctggagca ggagaagacc aggtctttgc agcagaacac acagctcaag 600
cgcttcatcc aggagctgag cggctcgtcc cccaagcgac ggcgggcaga gga caaggac 660
gaaggcatag gctccccgga catctgggag gacgagaagg cggaggacct gcggcgggag 720
atgattgagc tgcggcagca gctggacaag gagcgctcgg tgcgcatgat gctggaggag 780
caggtgcgct cgctggaggc ccacatgtac ccgaaaaagc tcaaggtgat tgcgcagcag 840

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gtgcagctgc agcagcagca ggaacaggtg aggtgctgc accaggagaa gctggagcgg 900
gaacagcagc agctgaggac ccagcttctg cccctccgg ccccccacca ccccccacg 960
gtgatcgtgc cagcaccgcc tcctcctccc tcccaccaca tcaatgtcgt caccatgggc 1020
ccctcctcgg tcatcaactc tgtttccaca tcccggcaaa atctggacac catc gtgcag 1080
gcaatccagc acatcgaggg ccccaggaa aagcaggagc tggaggagga gcagcggcga 1140
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gactccgagg cctcagacag tgacgccatg gaccagagcc gggaggagcc gtcgggggac 1260
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cactcaaccg gaggtcccg ggctgggggt tcgcagagct gtgggagcat cggca ccca 1500
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tgccaaaaag cattttttcc tttaaatatg ttttttaaga acagggaaaa ttaacaaaa 1620
ccccaggtta tttcttccct gccagagcc agcctgggat tgtcagcctt caatccctt 1680
tccttctctc ttttgggttt tc tttcttct cctttaagca cttacatggt tgggggttaag 1740
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gctgtgtgc cccctcccc cttcccatc tcggcactag aattcgccac tctccaccc 1860
cccagcccc acctctgct ccaggtctca tcttccacc caaaaatgtc tgtctc tctc 1920
tttttgtttt gtttgttgtt ggttttttat ttcttttttg tttgctttct gtttttgttt 1980
tgtttttctt ttttttctt cttttttttt tttttacaat tttgaggtct tcgtgttcaa 2040
ggagaagcta ttatatttt ttaagaaagt ggggagaaaa aaaaccaaga ggccaccgtg 2100
ccttgttaaa gaaacaaaat aaa gtttgta ctttgtttt taaaaaaaa 2149

```

&lt;210&gt; 461

&lt;211&gt; 6478

&lt;212&gt; ADN

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(6478)

&lt;223&gt; 3' terminal sequence

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(6478)

&lt;223&gt; Cyclin D2 (CCND2)

&lt;400&gt; 461

```

agagcgagca ggggagagcg agaccagttt taaggggagg accggtgcga gtaaggcagc 60
cccagggtc tgctcgcca ccaccaatc ctgcctccc ttctgctcca ccttctctct 120
ctgccctcac ctctcccccg aaaacccctt attagccaa aggaagg agg tcaggggaac 180
gctctccct ccccttcaa aaaacaaaa cagaaaaacc cttttccagg ccggggaaag 240
caggaggag aggggcccgc gggctggcca tggagctgct gtgccacgag gtggaccgg 300
tcgcagggc cgtgcccggac cgcaacctgc tccgagacga ccgcgtcctg cagaacctgc 360
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aactcaaaaga gaccgcccg ctgaccgcgg agaagctgtg catttacacc gacaactcca 660
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tctgtgggct ccagcaggat gaggaagtga gctcgtcac ttgtgatgcc ctgactgagc 960
tgctggctaa gatcaccaac acagacgtgg attgtctcaa agcttgcca g gagcagattg 1020
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cggaggatga actggacca gccagcacc ctacagacgt gcgggatatc gacctgtgag 1140  
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ttgtttttgt tctttg tgtt ttaggggtgaa acttaaaaaa aaaattctgc cccacactag 1260  
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tgagctagca catacaccoc cttgtagtat aatttcaagg aactgtgtac gccatttatg 1560  
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agggtattgg ctctgggtt tcatgttctg tgacatctct cttcttcttc caaatgcagt 1860  
tcattgcaga caccaccata ttgctatcta atggggaaat gtactgtatg gccataacca 1920  
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ggtcggttt tcaatcacac tgaattggca ggataagaaa aataggtcag ataagtatgg 3840  
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agtggagcag ccagcaagta agctagccag agttttctca agagccagct ttgctcagca 4080  
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tgagcttaaa cagaagcagc aaatgaaaga accggacaaa taaggaaagg cacaagccta 4260  
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ttctatctcg tcttacttc catctgtttg ttttttctc catcagtggt ggccgagttg 4680  
ttccccagc ctgccaattt ttgatcttc cctcttttg gccaaatcct agggggaaga 4740

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aatcctagta tgccaaaaat atatgctaag cataattaaa ctccatgcgg gtccata aca 4800
gccaaagaagc ctgcaggaga aagccaaggg cagttccctc cgcagaacac cccatgcgtg 4860
ctgagaggcg agctccttga agaaggggct gttcttccag gaggccttat tttgaactgc 4920
ctcaggaccc cactggagag cacagcatgc cttactactg ggtcatcctt ggtctatgtg 4980
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agtgacaaag ccagaggaga agacaaccct gacagcatca cgctgcatcc cattgctagc 5100
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ggcttctaag ccaaaaggat tcctc tttgt ttatctctga gacagtccaa ccttgagaat 5460
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gttcagtcag ccattocattt gtgcaaaata gggtagaag attcaagagg atatttatt a 5640
cttctcdata ccacatggct tttgatgatt ctggattcta aacaaccag aatggtcatt 5700
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ccctattctc ggctcagggt ttgagaagcc atcagcaaat gtgtacgtgc atgctgtagc 5820
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&lt;210&gt; 462

&lt;211&gt; 3490

&lt;212&gt; ADN

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(3490)

&lt;223&gt; 3' terminal sequence

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(3490)

&lt;223&gt; Junction plakoglobin (JUP)

&lt;400&gt; 462

```

cgccagagtc cggagcagcc gccgcccagc cgcgcgcagc tcagttcgt gtccgcgcgc 60
gtctccaccc cggcccagcc ccgaccggc ccggtcaggc ccatactca gtaggcacga 120
tgagggtgat gaacctgat gagcagccta tcaagggtgac tgagtggcag cagacataca 180
cttacgactc ggggtatccac tcgggcgcga acacctgcgt gccctccgtc agcagcaagg 240
gcatcatgga ggaggatgag gctgcgggc gccagtacac gctcaagaaa accaccactt 300
acaccaggg ggtgcccccc agccaagggt acctggagta ccagatgtcc acaacagcca 360
gggcaaaacg ggtgcgggag gccatgtgcc ctggtgtgtc ag gcaggagc agctcgcttc 420
tgctggccac ccagggtgag gggcaggcca ccaacctgca gcgactggcc gagccgtccc 480
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cagcccgctg caccaccagc atcctgcaca acctctccca ccaccgggag gggctgctcg 780
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ccccatttc ccgcacatgg tgtggggggc tgggggagg ccaagcagag tgttttatta 3420
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aataacacag                                     3490

```

&lt;210&gt; 463

&lt;211&gt; 1355

&lt;212&gt; ADN

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

<221> misc\_feature  
<222> (1)..(1355)  
<223> 3' terminal sequence

<220>  
<221> misc\_feature  
<222> (1)..(1355)  
<223> Growth arrest and DNA-damage-inducible, alpha  
(GADD45A)

<400> 463  
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cggctggcac aggaggagga gcccgggcgg gcgaggggcg gccggagagc gccagggcct 180  
gagctgccgg agcgggcgct gtgagtgagt gcagaaagca ggcgcccgcg cgctagccgt 240  
ggcaggagca gcccgcacgc cgcgtctctt ccctgggcga cctgcagttt gcaatatgac 300  
tttgaggaa ttctcggctg gagagcagaa gaccgaaagg atggataagg tgggggatgc 360  
cctggaggaa gtgctcagca aagccctgag tc agcgcacg atcactgtcg ggtgtacga 420  
agcgccaag ctgctcaacg tcgaccccgga taacgtggtg ttgtgcctgc tggcggcgga 480  
cgaggacgac gacagagatg tggctctgca gatccacttc accctgatcc aggcgttttg 540  
ctgcgagAAC gacatcaaca tcctgcgcgt cagcaaccgg ggccggctgg cggagctcct 600  
gctcttgagg accgacgtg gcccgcgggc gagcgagggc gccgagcagc ccccgacact 660  
gcactgcgtg ctggtgacga atccacattc atctcaatgg aaggatcctg ccttaagtca 720  
acttatttgt ttttgcggg aaagtgcgt catggatcaa tgggttccag tgattaatct 780  
ccctgaacgg tgatggcatc tgaatgaaaa taa ctgaacc aaattgcaact gaagtttttg 840  
aaataccttt gtagttactc aagcagttac tccctacact gatgcaagga ttacagaaac 900  
tgatgccaag gggctgagtg agttcaacta catgttctgg gggcccgag atagatgact 960  
ttgcagatgg aaagaggtga aaatgaagaa ggaagctgtg ttgaaacaga aaaataagtc 1020  
aaaaggaaca aaaattacaa agaaccatgc aggaaggaaa actatgtatt aatttagaat 1080  
ggttgagtta cattaaaata aaccaaatat gttaaagttt aagtgtgcag ccatagtttg 1140  
ggtatttttg gtttatatgc cctcaagtaa aagaaaagcc gaaagggtta atcatatttg 1200  
aaaaccatat tttattgtat tttgatgaga tatt aaattc tcaaagtttt attataaatt 1260  
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acctacaata aactggtatg aataattgca tcatt 1355

<210> 464  
<211> 732  
<212> ADN  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(732)  
<223> 3' terminal sequence

<220>  
<221> misc\_feature  
<222> (1)..(732)  
<223> Non-metastatic cells 1, protein (NM23A) expressed  
in (NME1)

<400> 464  
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aaacctaagc agctggaagg aaccatggcc aactgtgagc gtaccttcat tgcgatcaaa 120  
ccagatgggg tccagcgggg tcttgtggga gagattatca agcgttttga gcagaaagga 180  
ttccgccttg ttggtctgaa attcatgcaa gttccgaag atcttctcaa ggaacactac 240  
gttgacctga aggaccgtcc attctttgcc ggctggtga aatacatgca ctcagggccg 300

290/292

gtagttgcc a tggtctggga ggggctgaat gtggtgaaga cgggccgagt catgctcggg 360  
gagaccaacc ctgcagactc caagcctggg accatccgtg gagacttctg catacaagtt 420  
ggcaggaaca ttatacatgg cagtgattct gtggagagtg cagagaagga gatcggcttg 480  
tggtttcacc ctgaggaact ggtagattac acgagctgtg ctcagaactg gatctatgaa 540  
tgacaggagg gcagaccaca ttgcttttca catccatttc ccttccttcc catgggcaga 600  
ggaccaggct gtaggaaatc tagttattta caggaacttc atcataattt g gaggggaagc 660  
tcttgagct gtgagttctc cctgtacagt gttaccatcc ccgaccatct gattaaaatg 720  
cttcctcca gc

&lt;210&gt; 465

&lt;211&gt; 942

&lt;212&gt; ADN

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(942)

&lt;223&gt; 3' terminal sequence

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(942)

&lt;223&gt; Ribosomal protein L13 (RPL13) (ex BBC1)

&lt;400&gt; 465

ctttccgctc ggctgttttc ctgcgcagga gccgcagggc cgtaggcagc catggcgccc 60  
agccggaatg gcatgttctt gaagcccccac ttccacaagg actggcagcg gcgcgtggcc 120  
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cgccgcatcg ccccgcgccc cgcgtcgggt cccatccggc ccatcgtgcg ctgccccacg 240  
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aacaagtcca cggagtccct gcagaccaac gtgcagcggc tgaaggagta ccgctccaaa 420  
ctcatcctct tccccaggaa gccctcggcc cccaagaagg gagacagttc tgctgaagaa 480  
ctgaaactgg ccaccagct gaccggaccg gtcatgcccg tccggaacgt ctataagaag 540  
gagaaagctc gagtcatcac tgaggaagag aagaatttca aagccttcgc tagtctccgt 600  
atggcccgtg ccaacgcccg gctcttcggc atacgggcaa aaagagccaa ggaagccgca 660  
gaacaggatg ttgaaaagaa aaaataaagc cctcctgggg acttggaatc agtcgggcag 720  
tcatgtcggg tctccacgtg gtgtgtttcg tgggaacaac tgggcctggg atggggcttc 780  
actgctgtga cttcctcctg ccaggggatt tggggctttc ttgaaagaca gtccaagccc 840  
tgataaatgc tttactttct gtgttgaagc actgttggtt gtttggttag tgactgatgt 900  
aaaacggttt tcttgtgggg aggttacaga ggctgacttc ag 942

&lt;210&gt; 466

&lt;211&gt; 755

&lt;212&gt; ADN

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:primer

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)..(755)

&lt;223&gt; 3' terminal sequence

<220>  
<221> misc\_feature  
<222> (1)..(755)  
<223> vascular endothelial growth factor B (VEGFB)m

<400> 466  
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ccaggccctt gtctccagc ctgatgcccc tggccaccag aggaaagtgg tgtcatggat 120  
agatgtgtat actcgcgcta cctgccagcc ccgggaggtg gtggtgccct tgactgtgga 180  
gctcatgggc accgtggcca aacagctggt gccagctgc gtgactgtgc agcgtgtgg 240  
tggctgctgc cctgacgatg gcctggagtg tgtgccact gggcagcacc aagtccgat 300  
gcagatcctc atgatccggt acccgagcag t cagctgggg gagatgtccc tggagaaca 360  
cagccagtgt gaatgcagac ctaaaaaaaa ggacagtgtc gtgaagccag acagggtgc 420  
cactccccac caccgtcccc agccccgttc tgttccgggc tgggactctg cccccggagc 480  
accctcccca gctgacatca cccatccac tccagcccca ggccctctg cccacgtgc 540  
accagcacc accagcgccc tgacccccg acctgccgc gccgtgccg acgccgcagc 600  
ttctccgtt gccaaaggcg gggcttagag ctcaaccag acacctgcag gtgccggaag 660  
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cccagtgggg gaacaaagag gagcctggta aa aaa 755

<210> 467  
<211> 1039  
<212> ADN  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(1039)  
<223> 3' terminal sequence

<220>  
<221> misc\_feature  
<222> (1)..(1039)  
<223> Laminin receptor 1 (67kD, ribosomal protein SA)  
(LAMR1)

<400> 467  
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ggaggatgtc cttaa gttcc ttgcagcagg aaccactta ggtggcacca atcttgactt 180  
ccagatggaa cagtacatct ataaaaggaa aagtgatggc atctatatca taaatctcaa 240  
gaggacctgg gagaagcttc tgctggcagc tcgtgcaatt gttgccattg aaaaccctgc 300  
tgtgtcagt gttatatcct ccaggaatac tggccagagg gctgtgctg a agtttgctgc 360  
tgccactgga gccactcaa ttgctggccg cttcactcct ggaaccttca ctaaccagat 420  
ccaggcagcc ttccgggagc cagggcttct tgtggttact gacccaggg ctgaccacca 480  
gcctctcacg gaggcattct atgttaacct acctaccatt gcgtgtgta acacagattc 540  
tcctctgcgc tatgtg gaca ttgccatccc atgcaacaac aaggagctc actcagtggg 600  
tttaatgtgg tggatgctgg ctccgggaagt tctgcgcatg cgtggcacca ttcccgta 660  
acacccatgg gaggtcatgc ctgatctgta cttctacaga gatcctgaag agattgaaaa 720  
agaagagcag gctgctgctg agaaggcagt gaccaaggag gaatttcagg gtgaatggac 780  
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<211> 240  
<212> ADN  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<220>  
<221> misc\_feature  
<222> (1)..(240)  
<223> 3' terminal sequence

<220>  
<221> misc\_feature  
<222> (1)..(240)  
<223> Chorionic somatomammotropin hormone 1 (placental  
lactogen) = LACTOGEN Precursor

<400> 468  
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tccaggctcc cggaaagtc ctgatectgg nttttgncct nctctnactg ccctggnttn 180  
aanaagctng tgcntccaa ancgttcgt tatccagggt ttttgaccac gctatgctnc 240

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